TRANSLATED PROTEIN - NUCLEOTIDE 65 TO 598

```
   1 AATTCGGTACGAGGCTGGGGTTCAGGCGGGCAGCAGCTGCAGGCT

  46 GACCTTGCAGCTTGGCGGAATGGACTGGCCTCACAACCTGCTGTT
                            MetAspTrpProHisAsnLeuLeuPh

  91 TCTTCTTACCATTTCCATCTTCCTGGGGCTGGGCAGCCAGGAGCC
     eLeuLeuThrIleSerIlePheLeuGlyLeuGlySerGlnGluPr

 136 CCAAAAGCAAGAGGAAGGGGCAAGGGCGGCCTGGGCCCTGGCCTG
     oGlnLysGlnGluGluGlyAlaArgAlaAlaTrpAlaLeuAlaTr

 181 GCCTCACCAGGTGCCACTGGACCTGGTGTCACGGATGAAACCGTA
     pProHisGlnValProLeuAspLeuValSerArgMetLysProTy

 226 TGCCCGCATGGAGGAGTATGAGAGGAACATCGAGGAGATGGTGGC
     rAlaArgMetGluGluTyrGluArgAsnIleGluGluMetValAl

 271 CCAGCTGAGGAACAGCTCAGAGCTGGCCCAGAGAAAGTGTGAGGT
     aGlnLeuArgAsnSerSerGluLeuAlaGlnArgLysCysGluVa

 316 CAACTTGCAGCTGTGGATGTCCAACAAGAGGAGCCTGTCTCCCTG
     lAsnLeuGlnLeuTrpMetSerAsnLysArgSerLeuSerProTr

 361 GGGCTACAGCATCAACCACGACCCCAGCCGTATCCCCGTGGACCT
     pGlyTyrSerIleAsnHisAspProSerArgIleProValAspLe

 406 GCCGGAGGCACGGTGCCTGTGTCTGGGCTGTGTGAACCCCTTCAC
     uProGluAlaArgCysLeuCysLeuGlyCysValAsnProPheTh

 451 CATGCAGGAGGACCGCAGCATGGTGAGCGTGCCGGTGTTCAGCCA
     rMetGlnGluAspArgSerMetValSerValProValPheSerGl

 496 GGTTCCTGTGCGCCGCCGCCTCTGCCCGCCACCGCCCCGCACAGG
     nValProValArgArgArgLeuCysProProProProArgThrGl

 541 GCCTTGCCGCCAGCGCGCAGTCATGGAGACCATCGCTGTGGGCTG
     yProCysArgGlnArgAlaValMetGluThrIleAlaValGlyCy

 586 CACCTGCATCTTCTGAATCACCTGGCCCAGAAGCCAGGCCAGCAG
     sThrCysIlePhe

 631 CCCGAGACCATCCTCCTTGCACCTTTGTGCCAAGAAAGGCCTATG
 676 AAAAGTAAACACTGACTTTTGAAAGCAAAAAAACCCCAGGAAGCT
 721 TCGGCTGGGTTCCAGACACATGGAAAACAGACTTCCTGTGCCAGC
 766 GCATGCTGATCCCTTCAGCAGCCGCTTCTCCACCCTTGGGGCTGC
 811 TCTCCAGCACCTGGCAGTGTCCAGAGCGGATAGGGGCGCCGTGTT
 856 TGGTGAATGAGTGCACAGACGCCTCTAGGGGGAGCCCAAGATCTG
 901 CCTCCTGCCTCCCTCTATTATGCCTTCATAGGTGGGTCAGAACAA
 946 AGAATTCCTTATCAACCTCCCGGGTCCCCCACTGCCAATCACCCA
 991 CCTCCATTCTACCCTCTACAGCTGCCCCTTATCCCCCAAAGTCCT
1036 GAAATTTTGCTTGGGTCACCTGCTCCAGGAGGCAGAGTTCCCATG
1081 AAGGGTATTAAACGTCTACTACACTGC
```

Fig. 1

TRANSLATED PROTEIN - NUCLEOTIDE 92 TO 1123

```
  1 CAAGCTTGAGAGCAACACAATCTATCAGGAAAGAAAGAAAGAAAA
 46 AAACCGAACCTGACAAAAAAGAAGAAAAAGAAGAAGAAAAAAAAT

 91 CATGAAAACCATCCAGCCAAAAATGCACAATTCTATCTCTTGGGC
    MetLysThrIleGlnProLysMetHlsAsnSerIleSerTrpAl

136 AATCTTCACGGGGCTGGCTGCTCTGTGTCTCTTCCAAGGAGTGCC
    aIlePheThrGlyLeuAlaAlaLeuCysLeuPheGlnGlyValPr

181 CGTGCGCAGCGGAGATGCCACCTTCCCCAAAGCTATGGACAACGT
    oValArgSerGlyAspAlaThrPheProLysAlaMetAspAsnVa

226 GACGGTCCGGCAGGGGGAGAGCGCCACCCTCAGGTGCACTATTGA
    lThrValArgGlnGlyGluSerAlaThrLeuArgCysThrIleAs

271 CAACCGGGTCACCCGGGTGGCCTGGCTAAACCGCAGCACCATCCT
    pAsnArgValThrArgvalAlaTrpLeuAsnArgSerThrIleLe

316 CTATGCTGGGAATGACAAGTGGTGCCTGGATCCTCGCGTGGTCCT
    uTyrAlaGlyAsnAspLysTrpCysLeuAspProArgValValLe

361 TCTGAGCAACACCCAAACGCAGTACAGCATCGAGATCCAGAACGT
    uLeuSerAsnThrGlnThrGlnTyrSerIleGluIleGlnAsnVa

406 GGATGTGTATGACGAGGGCCCTTACACCTGCTCGGTGCAGACAGA
    lAspValTyrAspGluGlyProTyrThrCysSerValGlnThrAs

451 CAACCACCCAAAGACCTCTAGGGTCCACCTCATTGTGCAAGTATC
    pAsnHisProLysThrSerArgValHisLeuIleValGlnValSe

496 TCCCAAAATTGTAGAGATTTCTTCAGATATCTCCATTAATGAAGG
    rProLysIleValGluIleSerSerAspIleSerIleAsnGluGl

541 GAACAATATTAGCCTCACCTGCATAGCAACTGGTAGACCAGAGCC
    yAsnAsnIleSerLeuThrCysIleAlaThrGlyArgProGluPr

586 TACGGTTACTTGGAGACACATCTCTCCCAAAGCGGTTGGCTTTGT
    oThrValThrTrpArgHisIleSerProLysAlaValGlyPheVa

631 GAGTGAAGACGAATACTTGGAAATTCAGGGCATCACCCGGGAGCA
    lSerGluAspGluTyrLeuGluIleGlnGlyIleThrArgGluGl

676 GTCAGGGGACTACGAGTGCAGTGCCTCCAATGACGTGGCCGCGCC
    nSerGlyAspTyrGluCysSerAlaSerAsnAspValAlaAlaPr
```

Fig. 2

```
721  CGTGGTACGGAGAGTAAAGGTCACCGTGAACTATCCACCATACAT
     oValValArgArgValLysValThrValAsnTyrProProTyrIl

766  TTCAGAAGCCAAGGGTACAGGTGTCCCCGTGGGACAAAAGGGGAC
     eSerGluAlaLysGlyThrGlyValProValGlyGlnLysGlyTh

811  ACTGCAGTGTGAAGCCTCAGCAGTCCCCTCAGCAGAATTCCAGTG
     rLeuGlnCysGluAlaSerAlaValProSerAlaGluPheGlnTr

856  GTACAAGGATGACAAAAGACTGATTGAAGGAAAGAAAGGGGTGAA
     pTyrLysAspAspLysArgLeuIleGluGlyLysLysGlyValLy

901  AGTGGAAAACAGACCTTTCCTCTCAAAACTCATCTTCTTCAATGT
     sValGluAsnArgProPheLeuSerLysLeuIlePhePheAsnVa

946  CTCTGAACATGACTATGGGAACTACACTTGCGTGGCCTCCAACAA
     lSerGluHisAspTyrGlyAsnTyrThrCysValAlaSerAsnLy

991  GCTGGGCCACACCAATGCCAGCATCATGCTATTTGGTCCAGGCGC
     sLeuGlyHisThrAsnAlaSerIleMetLeuPheGlyProGlyAl

1036 CGTCAGCGAGGTGAGCAACGGCACGTCGAGGAGGGCAGGCTGCGT
     aValSerGluValSerAsnGlyThrSerArgArgAlaGlyCysVa

1081 CTGGCTGCCGCCTCTTCTGGTCTTGCACCTGCTTCTCAAATTTTG
     lTrpLeuProProLeuLeuValLeuHisLeuLeuLeuLysPhe

1126 ATGTGAGTGCCACTTCCCCACCCGGGAAAGGCTGCCGCCACCACC
1171 ACCACCAACACAACAGCAATGGCAACACCGACAGCAACCAATCAG
1216 ATATATACAAATGAAATTAGAAGAAACACAGCCTCATGGGACAGA
1261 AATTTGAGGGAGGGGAACAAAGAATACTTTGGGGGGAAAAGAGTT
1306 TTAAAAAAGAAATTGAAAATTGCCTTGCAGATATTTAGGTACAAT
1351 GGAGTTTTCTTTTCCCAAACGGGAAGAACACAGCACACCCGGCTT
1396 GGACCCACTGCAAGCTGCATCGTGCAACCTCTTTGGTGCCAGTGT
1441 GGGCAAGGGCTCAGCCTCTCTGCCCACAGAGTGCCCCCACGTGGA
1486 ACATTCTGGAGCTGGCCATCCCAAATTCAATCAGTCCATAGAGAC
1531 GAACAGAATGAGACCTTCCGGCCCAAGCGTGGCGCTGCGGGCACT
1576 TTGGTAGACTGTGCCACCACGGCGTGTG
```

Fig. 2 (continued)

TRANSLATED PROTEIN - FRAME: 3 - NUCLEOTIDE 501 TO 1532

```
1
GCCAGGGAATGCCAGGGGGAAAGGGATTTTCTGATACTCAGAAGA
46
CTCAGAGACTGTCAGTTTAAAAAATGAAAGTAATATAGAAGGGGC
91
AAAGTGGCATTTATCATTCTATCTCTCCAGGCTCCTGTCTCTTTA
136
ATCAGCTAGCCTGATTTGCCCAGTAAATGATTCCTGAGAGTGTGT
181
GTGCGTGTGTGTGTGTGTGTGTGCCCGCGCGTGTGTTGTAGCT
226
CTGTCAATCCTTGGATTAGAACCAATGATTGCAGCTTGTAAGAGG
271
GCTGTCCAGGGCCAGATTGTACAATGTGTCTCAGTGCCAGAGTAT
316
GAGTGGAGATAATTACGGAGAAGTCATACTCTCTCACACCCTCGG
361
CTTTCTTGTTGTGTCCTTCAGCAAAACAGTGGATTTAAATCTCCT
406
TGCACAAGCTTGAGAGCAACACAATCTATCAGGAAAGAAAGAAAG
451
AAAAAAACCGAACCTGACAAAAAAGAAGAAAAAGAAGAAGAAAAA
496
AAATCATGAAAACCATCCAGCCAAAAATGCACAATTCTATCTCTT
     MetLysThrIleGlnProLysMetHisAsnSerIleSerT
541
GGGCAATCTTCACGGGGCTGGCTGCTCTGTGTCTCTTCCAAGGAG
rpAlaIlePheThrGlyLeuAlaAlaLeuCysLeuPheGlnGlyV
586
TGCCCGTGCGCAGCGGAGATGCCACCTTCCCCAAAGCTATGGACA
alProValArgSerGlyAspAlaThrPheProLysAlaMetAspA
631
ACGTGACGGTCCGGCAGGGGGAGAGCGCCACCCTCAGGTGCACTA
snValThrValArgGlnGlyGluSerAlaThrLeuArgCysThrI
676
TTGACAACCGGGTCACCCGGGTGGCCTGGCTAAACCGCAGCACCA
leAspAsnArgvalThrArgvalAlaTrpLeuAsnArgSerThrI
721
TCCTCTATGCTGGGAATGACAAGTGGTGCCTGGATCCTCGCGTGG
leLeuTyrAlaGlyAsnAspLysTrpCysLeuAspProArgValV
766
TCCTTCTGAGCAACACCCAAACGCAGTACAGCATCGAGATCCAGA
alLeuLeuSerAsnThrGlnThrGlnTyrSerIleGluIleGlnA
811
ACGTGGATGTGTATGACGAGGGCCCTTACACCTGCTCGGTGCAGA
snValAspValTyrAspGluGlyProTyrThrCysSerValGlnT
856
CAGACAACCACCCAAAGACCTCTAGGGTCCACCTCATTGTGCAAG
hrAspAsnHisProLysThrSerArgValHisLeuIleValGlnV
```

Fig. 3

901
TATCTCCCAAAATTGTAGAGATTTCTTCAGATATCTCCATTAATG
alSerProLysIleValGluIleSerSerAspIleSerIleAsnG
946
AAGGGAACAATATTAGCCTCACCTGCATAGCAACTGGTAGACCAG
luGlyAsnAsnIleSerLeuThrCysIleAlaThrGlyArgProG
991
AGCCTACGGTTACTTGGAGACACATCTCTCCCAAAGCGGTTGGCT
luProThrValThrTrpArgHisIleSerProLysAlaValGlyP
1036
TTGTGAGTGAAGACGAATACTTGGAAATTCAGGGCATCACCCGGG
heValSerGluAspGluTyrLeuGluIleGlnGlyIleThrArgG
1081
AGCAGTCAGGGGACTACGAGTGCAGTGCCTCCAATGACGTGGCCG
luGlnSerGlyAspTyrGluCysSerAlaSerAsnAspValAlaA
1126
CGCCCGTGGTACGGAGAGTAAAGGTCACCGTGAACTATCCACCAT
laProValValArgArgvalLysValThrValAsnTyrProProT
1171
ACATTTCAGAAGCCAAGGGTACAGGTGTCCCCGTGGGACAAAAGG
yrIleSerGluAlaLysGlyThrGlyValProValGlyGlnLysG
1216
GGACACTGCAGTGTGAAGCCTCAGCAGTCCCCTCAGCAGAATTCC
lyThrLeuGlnCysGluAlaSerAlaValProSerAlaGluPheG
1261
AGTGGTACAAGGATGACAAAAGACTGATTGAAGGAAAGAAAGGGG
lnTrpTyrLysAspAspLysArgLeuIleGluGlyLysLysGlyV
1306
TGAAAGTGGAAAACAGACCTTTCCTCTCAAAACTCATCTTCTTCA
alLysValGluAsnArgProPheLeuSerLysLeuIlePhePheA
1351
ATGTCTCTGAACATGACTATGGGAACTACACTTGCGTGGCCTCCA
snValSerGluHisAspTyrGlyAsnTyrThrCysValAlaSerA
1396
ACAAGCTGGGCCACACCAATGCCAGCATCATGCTATTTGGTCCAG
snLysLeuGlyHisThrAsnAlaSerIleMetLeuPheGlyProG
1441
GCGCCGTCAGCGAGGTGAGCAACGGCACGTCGAGGAGGGCAGGCT
lyAlaValSerGluValSerAsnGlyThrSerArgArgAlaGlyC
1486
GCGTCTGGCTGCCGCCTCTTCTGGTCTTGCACCTGCTTCTCAAAT
ysValTrpLeuProProLeuLeuValLeuHisLeuLeuLeuLysP
1531
TTTGATGTGAGTGCCACTTCCCCACCCGGGAAAGGCTGCCGCCAC
he

Fig. 3 (continued)

1576
CACCACCACCAACACAACAGCAATGGCAACACCGACAGCAACCAA
1621
TCAGATATATACAAATGAAATTAGAAGAAACACAGCCTCATGGGA
1666
CAGAAATTTGAGGGAGGGGAACAAAGAATACTTTGGGGGGAAAAG
1711
AGTTTTAAAAAAGAAATTGAAAATTGCCTTGCAGATATTTAGGTA
1756
CAATGGAGTTTTCTTTTCCCAAACGGGAAGAACACAGCACACCCG
1801
GCTTGGACCCACTGCAAGCTGCATCGTGCAACCTCTTTGGTGCCA
1846
GTGTGGGCAAGGGCTCAGCCTCTCTGCCCACAGAGTGCCCCCACG
1891
TGGAACATTCTGGAGCTGGCCATCCCAAATTCAATCAGTCCATAG
1936
AGACGAACAGAATGAGACCTTCCGGCCCAAGCGTGGCGCTGCGGG
1981
CACTTTGGTAGACTGTGCCACCACGGCGTGTG

Fig. 3 (continued)

TRANSLATED PROTEIN - NUCLEOTIDE 529 TO 1026

```
   1 GCTCTTCCTGAAGGAAGATCCAGTGGCATATCTCCATGGCTGCCA
  46 GACAGAGTAGAGAAATGGAACTTATCGGTGTCTCTTCAGAAGTTT
  91 TGTTACAAATATCCAGAAATATTTCTATAATCTAATCAGCAGATT
 136 ATGAATATATGCATTAGACTTTAGTTTTGGTGCAATCACATGAAT
 181 TCCATTTTGTGGAGTAAGAGGTGACTGGGGTATAGGGTACAACCC
 226 ATAGCCATCCATGTTCATCTTTGTTTTGAATATAATTGGCTAGAA
 271 GATATACATATATCTATGTAACTTCCTCTAGCATCCTCCAGTATG
 316 GAGGCTGCATTAAGACTGCATGAAGGAGAGGGAGAGAAGGGAGAA
 361 ACAGAGCAGCTGGACAAGAGGACAGGTATAGGGAATAAGGGAGAA
 406 GCCAGTAAGGCAGGAAAGACCCTCCGTGACAAAGGGGCAGGGAAC
 451 AGAACTCAAACATTTAATGGCAGGTAACCCAGGTTAGAATGGTAA

 496 ATTGAAAGGTGAATATAAAGGGAGAATGGTGAAATGAATTTTCTG
                                         MetAsnSheLeu

 541 AAATTAATTGCTGTGTTTATAGTTTTTAGCCATGCATCGGAATCA
     LysLeuIleAlaValPheIleValPheSerHisAlaSerGluSer

 586 CCTCAGGACTCCACTCCCAATCAATTATATATCTGGGGGAGGACC
     ProGlnAspSerThrProAsnGlnLeuTyrIleTrpGlyArgThr

 631 AAGGCGTTGGTATTTTTCAGAAGCTCCACTGGTGATTCTGACAGC
     LysAlaLeuValPhePheArgSerSerThrGlyAspSerAspSer

 676 ACAGCTAGGATTAAGAAACTGATCAATGGGAACGGCATGCCTGTT
     ThrAlaArgIleLysLysLeuIleAsnGlyAsnGlyMetProVal

 721 GCAGAGGAGCTTCCCTGGGAAATGTCACACACAGAACATCAATCT
     AlaGluGluLeuProTrpGluMetSerHisThrGluHisGlnSer

 766 TCCTTCCCCACTCCTGAGATCCCTCATTCTTTGGCACCAGGAACA
     SerPheProThrProGluIleProHisSerLeuAlaProGlyThr

 811 GTTGCAATTAGTAAACCCTGGTTCCCTGCTGTCTCACAAATCGCA
     ValAlaIleSerLysProTrpPheProAlaValSerGlnIleAla

 856 AGAGTCCAACGTGTGGATATAAACTTTTGTTCATGGGAGGATCTT
     ArgValGlnArgValAspIleAsnPheCysSerTrpGluAspLeu

 901 TCTCCCAGTGGAAAAGCAACTGGGAAAAGCAGGACACACTGCACA
     SerProSerGlyLysAlaThrGlyLysSerArgThrHisCysThr

 946 GTGACTGCAGTTTCATCCAATGCCACCACCCATGCAGGCATAAAT
     ValThrAlaValSerSerAsnAlaThrThrHisAlaGlyIleAsn

 991 AATGAACATGGATGGGGGAGTCTGGAGCTGCTGAATTGAGGAAGA
     AsnGluHisGlyTrpGlySerLeuGluLeuLeuAsn

1036 AAGAACACAGAAATTAAAATTCTCACAAAGGTTACCATTAAGCTA
1081 GAGGAAGACCACACCACTGTGTGTCCACAAAGATACAGAGCCAGG
1126 CCGGGTTCAGCCATGCTGGTCATCTGCTCTATATAATACAATTAT
1171 TTAGAGATGGTGGGTAGAGAACAACTACAGAAAAAAAAAAAAAAA
1216 AAAAAAAAAAAAA
```

Fig. 4

TRANSLATED PROTEIN - NUCLEOTIDE 410 TO 889

```
  1 ACGCGTCACATAAAGGAAAGATACGTTTTAATCATCTTTACAAGT
 46 GCGTCCTTGTACCTTTCGGGATAACCTGTACTGATTTCTCTGCAG
 91 GACCTTTTCAAAGAATCCTCTTCAAGAGAGAAACAAATTTTAGGC
136 TGACGACTTCACGGAGAGGCAGGTTCTGCTGTTGCCAATGAACGA
181 GAACTTTCTACTAGGCTGGCGGCATGCAGAGCCCACGTCTGTCAG
226 CTGCCACCTTCGTAAAGCACACGTTTCACATGCATGAGCTCGAGT
271 GGCTAGAACTTCAAAACTGTGCTCAGGTTTTTGTTTTGGAAGTTA
316 TAAAAAAGTTGCTCACAAACAATAGTTATTGCCTTTTATATCTTT
361 TATGTTAGTCTACTAGTCAGCATTCTGCCCAAAATGGAAAGCCAC

406 TCCCATGGGAAGGGAGGGGGTAGCAGCTGGGAGTCTGCTCTTCCA
         MetGlyArgGluGlyValAlaAlaGlySerLeuLeuPheGl

451 GCTGGGGGCCCTCCCACCCCCATGGGGAGGAAAGACGTCAAGCTC
    nLeuGlyAlaLeuProProProTrpGlyGlyLysThrSerSerSe

496 CAGCCACTGGCCCCGGTGGGTCCCAAAGCCCCACCCCTCATGCTC
    rSerHisTrpProArgTrpValProLysProHisProSerCysSe

541 TCCTCTGGTCACCTCTATTTACGCTCACATGCCCCTTCCTGTCCT
    rProLeuValThrSerIleTyrAlaHisMetProLeuProValLe

586 TCACCTGCACGTCACCAGCAGGTCCCGCCAACCCCAAATCTATCT
    uHisLeuHisValThrSerArgSerArgGlnProGlnIleTyrLe

631 GGTGAAAAACCTGGAGAACAAGAGCGGAGTCTAAGAGAGATGTAAA
    uValLysThrTrpArgThrArgAlaGluSerLysArgAspValAs

676 TGAAAACACAGATCAACAGACACACCAGAAGGGAAGCGTTGTTTC
    nGluAsnThrAspGlnGlnThrHisGlnLysGlySerValValSe

721 CGCGGGGAAAGGAGATGGAAAGGGGAAGAGAAGTGAAGAATTCTG
    rAlaGlyLysGlyAspGlyLysGlyLysArgSerGluGluPheCy

766 CGCCCGAAGCTCGGGTTGGTGTTTGCTCAACTGCTTTACTCATTT
    sAlaArgSerSerGlyTrpCysLeuLeuAsnCysPheThrHisPh

811 TAACCCTTTCACCTATCCTGGGAGAAACCCAGGCTTGTCACCTTT
    eAsnProPheThrTyrProGlyArgAsnProGlyLeuSerProPh

856 TCATGTTGGGTTGTTTGTTTATTGGCCTCTTAAGTGAGAATTGAT
    eHisValGlyLeuPheValTyrTrpProLeuLys

901 CCGTGAAGGGAAACAGACAGGAGGAGGTCAGATTGCGAATACCTG
946 GGGCTTCCTAGGGTCCAGTGCGGCAGTTACCGCACCTGCCTTCAC
991 CGGTGAACCTTTAGCCAGCTGAACAACCACCAAAGCGCCCTGCAG
```

Fig. 5

```
1036 AGACAAGTCATCCAGCCCTCTGGCATGTCCCTGGTAGCCCGGGCA
1081 CCAGCCGCTGCGGCTTGTGAGGGGCACCATGCTCCACCCCACGGG
1126 GACCTTCACAGTTGGAAAAAAGAAGAGGAAAAACTAATTCCTTCG
1171 GTAACAGTTTATTTTCATTTTTGGGAAAGGCAAAACCACTACCTG
1216 GAACTCGGTGCCTCCGTGGTTAACTTTCCTATTTTGCTTGTGATT
1261 TAAAGGCTGTTCTGGGTCAGGGGGGAAAAGGTGTCTCCTTCGGTA
1306 GGGAATATATAACGTGGTGATAACCTGTCACTAGGCAGAAGCATC
1351 CACTCTGCAGGGACAGTGGCCCCTCAGGAAAGCCCGCCGCTCCTG
1396 GCCAAGGCCTCTCTGCAGACTCCACGGGGGCTCACCCTCTGCCGT
1441 CAGGCGACTCTGAAATTCCGACATTTCTCCCTTAAAGTCTCAACA
1486 GACACAAGAGAAGTTTCCATCAAGCAAGCACTGACATATTTATAT
1531 TAAAAAATAGTGCAAAATCTCAACATTTATATAAATAACTCTAAA
1576 CCCCTGCTTTGTAATTTTTTTCTTTACAAGGTAATACACACTTTC
1621 TGACTTGGCACTCAAAAATTGCCATTTTTTTCCTCTTCTAGTTCA
1666 GAAAACAACTTTTTTTTTTAATAGGCCTCTTCTAATACAAAAATA
1711 CTCCTGCCCTCGCACATACAGTTTCTCTTATCTTATATATATTTA
1756 TATATATAATATTGCAGATCTTTAAACAAAGGTTTTGTGCAAATA
1801 TGTCTTTAAAGTTAAGTGAAATTATCATAAACAAAAGAAAATAAG
1846 CATTCACGCACGCAGCTCAACTAGAAACAAGAAAGACTACTGTAG
1891 AAATTTTTTTTCTTTTGCCTTCAAGAC
```

Fig. 5 (continued)

TRANSLATED PROTEIN - NUCLEOTIDE 410 TO 892

```
   1 ACGCGTCACATAAAGGAAAGATACGTTTTAATCATCTTTACAAGT
  46 GCGTCCTTGTACCTTTCGGGATAACCTGTACTGATTTCTCTGCAG
  91 GACCTTTTCAAAGAATCCTCTTCAAGAGAGAAACAAATTTTAGGC
 136 TGACGACTTCACGGAGAGGCAGGTTCTGCTGTTGCCAATGAACGA
 181 GAACTTTCTACTAGGCTGGCGGCATGCAGAGCCCACGTCTGTCAG
 226 CTGCCACCTTCGTAAAGCACACGTTTCACATGCATGAGCTCGAGT
 271 GGCTAGAACTTCAAAACTGTGCTCAGGTTTTTGTTTTGGAAGTTA
 316 TAAAAAAGTTGCTCACAAACAATAGTTATTGCCTTTTATATCTTT
 361 TATGTTAGTCTACTAGTCAGCATTCTGCCCAAAATGGAAAGCCAC

 406 TCCCATGGGAAGGGAGGGGGTAGCAGCTGGGAGTCTGCTCTTCCA
         MetGlyArgGluGlyValAlaAlaGlySerLeuLeuPheGl

 451 GCTGGGGGCCCTCCCACCCCCATGGGGAGGAAAGACGTCAAGCTC
     nLeuGlyAlaLeuProProProTrpGlyGlyLysThrSerSerSe

 496 CAGCCACTGGCCCCGGTGGGTCCCAAAGCCCCACCCCTCATGCTC
     rSerHisTrpProArgTrpValProLysProHisProSerCysSe

 541 TCCTCTGGTCACCTCTATTTACGCTCACATGCCCCTTCCTGTCCT
     rProLeuValThrSerIleTyrAlaHisMetProLeuProValLe

 586 TCACCTGCACGTCACCAGCAGGTCCCGCCAACCCCAAATCTATCT
     uHisLeuHisvalThrSerArgSerArgGlnProGlnIleTyrLe

 631 GGTGAAAACCTGGAGAACAAGAGCGGAGTCTAAGAGAGATGTAAA
     uValLysThrTrpArgThrArgAlaGluSerLysArgAspValAs

 676 TGAAAACACAGATCAACAGACACACCAGAAGGGAAGCGTTGTTTC
     nGluAsnThrAspGlnGlnThrHisGlnLysGlySerValValSe

 721 CGCGGGGAAAGGAGATGGAAAGGGGAAGAGAAGTGAAGAATTCTG
     rAlaGlyLysGlyAspGlyLysGlyLysArgSerGluGluPheCy

 766 CGCCCGAAGCTCGGGTTGGTGTTTGCTCAACTGCTTTACTCATTT
     sAlaArgSerSerGlyTrpCysLeuLeuAsnCysPheThrHisPh

 811 TAACCCTTTCACCTATCCTGGGAGAAACCCAGGCTTGTCACCTTT
     eAsnProPheThrTyrProGlyArgAsnProGlyLeuSerProPh

 856 TCATGTTGGGTTGTTTATTGGCCTCTTAAGTGAGAATTGATCCGT
     eHisValGlyLeuPheIleGlyLeuLeuSerGluAsn

 901 GAAGGGAAACAGACAGGAGGAGGTCAGATTGCGAATACCTGGGGC
 946 TTCCTAGGGTCCAGTGCGGCAGTTACCGCACCTGCCTTCACCGGT
 991 GAACCTTTAGCCAGCTGAACAACCACCAAAGCGCCCTGCAGAGAC
1036 AAGTCATCGAGCCCTCTGGCATGTCCCTGGTAGCCCGGGCACCAG
1081 CCGCTGCGGCTTGTGAGGGGCACCATGCTCCACCCCACGGGGACC
1126 TTCACAGTTGGAAAAAAGAAGAGGAAAAACTAATTCCTTCGGTAA
1171 CAGTTTATTTTCATTTTTGGGAAAGGCAAAACCACTACCTGGAAC
1216 TCGGTGCCTGNGANNTCTTANNTNCTNNCTNAGNCNNATNNGNNA
1261 NNNNTNNNNNANNCTTNNA
```

Fig. 6

TRANSLATED PROTEIN - NUCLEOTIDE 199 TO 1146

```
  1 TAGAATTCAGCGGCCGCTTAATTCTAGAACGAATGCCAGTGCCTG
 46 GAGGCATGCAGGCCCAGCTACGTGCCTGTGTGCGGCTCTGATGGG
 91 AGGTTTTATGAAAACCACTGTAAGCTCCACCGTGCTGCTTGCCTC
136 CTGGGAAAGAGGATCACCGTCATCCACAGCAAGGACTGTTTCCTC

181 AAAGGTGACACGTGCACCATGGCCGGCTACGCCCGCTTGAAGAAT
                                      MetAlaGlyTyrAlaArgLeuLysAsn

226 GTCCTTCTGGCACTCCAGACCCGTCTGCAGCCACTCCAAGAAGGA
    ValLeuLeuAlaLeuGlnThrArgLeuGlnProLeuGlnGluGly

271 GACAGCAGACAAGACCCTGCCTCCCAGAAGCGCCTCCTGGTGGAA
    AspSerArgGlnAspProAlaSerGlnLysArgLeuLeuValGlu

316 TCTCTGTTCAGGGACTTAGATGCAGATGGCAATGGCCACCTCAGC
    SerLeuPheArgAspLeuAspAlaAspGlyAsnGlyHisLeuSer

361 AGCTCCGAACTGGCTCAGCATGTGCTGAAGAAGCAGGACCTGGAT
    SerSerGluLeuAlaGlnHisValLeuLysLysGlnAspLeuAsp

406 GAAGACTTACTTGGTTGCTCACCAGGTGACCTCCTCCGATTTGAC
    GluAspLeuLeuGlyCysSerProGlyAspLeuLeuArgPheAsp

451 GATTACAACAGTGACAGCTCCCTGACCCTCCGCGAGTTCTACATG
    AspTyrAsnSerAspSerSerLeuThrLeuArgGluPheTyrMet

496 GCCTTCCAAGTGGTTCAGCTCAGCCTCGCCCCCGAGGACAGGGTC
    AlaPheGlnValValGlnLeuSerLeuAlaProGluAspArgVal

541 AGTGTGACCACAGTGACCGTGGGGCTGAGCACAGTGCTGACCTGC
    SerValThrThrValThrValGlyLeuSerThrValLeuThrCys

586 GCCGTCCATGGAGACCTGAGGCCACCAATCATCTGGAAGCGCAAC
    AlaValHisGlyAspLeuArgProProIleIleTrpLysArgAsn

631 GGGCTCACCCTGAACTTCCTGGACTTGGAAGACATCAATGACTTT
    GlyLeuThrLeuAsnPheLeuAspLeuGluAspIleAsnAspShe

676 GGAGAGGATGATTCCCTGTACATCACCAAGGTGACCACCATCCAC
    GlyGluAspAspSerLeuTyrIleThrLysValThrThrIleHis

721 ATGGGCAATTACACCTGCCATGCTTCCGGCCACGAGCAGCTGTTC
    MetGlyAsnTyrThrCysHisAlaSerGlyHisGluGlnLeuPhe

766 CAGACCCACGTCCTGCAGGTGAATGTGCCGCCAGTCATCCGTGTC
    GlnThrHisValLeuGlnValAsnValProProValIleArgVal
```

Fig. 7

811 TATCCAGAGAGCCAGGCACAGGAGCCTGGAGTGGCAGCCAGCCTA
TyrProGluSerGlnAlaGlnGluProGlyValAlaAlaSerLeu

856 AGATGCCATGCTGAGGGCATTCCCATGCCCAGAATCACTTGGCTG
ArgCysHisAlaGluGlyIleProMetProArgIleThrTrpLeu

901 AAAAACGGCGTGGATGTCTCAACTCAGATGTCCAAACAGCTCTCC
LysAsnGlyValAspValSerThrGlnMetSerLysGlnLeuSer

946 CTTTTAGCCAATGGGAGCGAACTCCACATCAGCAGTGTTCGGTAT
LeuLeuAlaAsnGlySerGluLeuHisIleSerSerValArgTyr

991 GAAGACACAGGGGCATACACCTGCATTGCCAAAAATGAAGTGGGT
GluAspThrGlyAlaTyrThrCysIleAlaLysAsnGluValGly

1036 GTGGATGAAGATATCTCCTCGCTCTTCATTGAAGACTCAGCTAGA
ValAspGluAspIleSerSerLeuPheIleGluAspSerAlaArg

1081 AAGACCCTTGCAAACATCCTGTGGCGAGAGGAAGGTACCAAGCTT
LysThrLeuAlaAsnIleLeuTrpArgGluGluGlyThrLysLeu

1126 CATTGTTTTGCGTCATGCCTGTGATCACGTGTGTTTGGTTCTATG
HisCysPheAlaSerCysLeu

1171 ATGGGCCGTCTTTCCATGATCTGCCACCAGCTTTCCCACACAAAG
1216 CAGCCCTATGGGAGCAGGAAGTCAATGTCAAATTCAAGTGGCATA
1261 TGCATTGAATCAAATTTAAAATGTACTCCTGTCTTTAATGAGAAA
1306 TTTTTAAATGCAAAGCTTTCATTAAAAGTGGCTTGTAACCTCTGC
1351 TGAAGCAGAACAGTTGGTAAGGGTTCCTGGTCAGATCTGGGCCTT
1396 AAACTTTTTTCCAGTAGCTGACTGGTGTTGGGTTTAGTGTTTTGC
1441 CTATCTTGTGTGGTTTTAAAAAGACAAAACAAGTTGTAGATCTCT
1486 ACTAGATAGTCACTGTACCTTAAATATGCTTTGATTGAGGAAAAC
1531 CCGAGGAAAAAGCTGCCATGATTTCTGCCAATGTATATTTTTAAA
1576 TGTATAGATGTTTAGAAACATATTTATCAAGCAAATCTTTAGTAA
1621 GTTGAGCCATATGAAGTTGCCATTTTTGTGCATCAAAGTGGTCTA
1666 AGATTGACAATTTCATATGGCTGA

Fig. 7 (continued)

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   1 GGAGAGGGCTGCATTGCTGTTGCTCACTGACCTTCTTTTATGCTGGCCTTTGGTTCAGAATGGCACATCATTCCTCGTTT
  81 TTGGCCCTCCAGCTGAACACCTGTTCTCTGTGGCACTGACTCCTCTTTCCATAGGGACATCATACAACAGTCGCCTTTAT
 161 CTGAGGTTGTGCAAAGAGGGATGGAGGAGAAAACAATGGAGAATCCCTGGCAGATTTCCCCAGGACGAGAGAAGGATATC
 241 CAATTGCTCATCAGGGAAGGTGCTAGGTCTCCCAGCCAGACGCCCTCAGAGGCCGGTGTCAAGTCTCCCTCACCTCTGTG
 321 ATGTGAAGTCAGCTCGTTCATGACCTGGGCAGGCAGAGGGTCAGAGGGGCAGATGGAGCACTCCTGGCCTGATGAAGACT
 401 CATCAAAATGAAACCAGGAGGCTTTTGGCTGCATCTCACACTGCTCGGAGCCTCCCTGCCGGCTGCGCTGGGATGGATGG
              MetLysProGlyGlyPheTrpLeuHisLeuThrLeuLeuGlyAlaSerLeuProAlaAlaLeuGlyTrpMetA
 481 ACCCAGGAACCAGCAGAGGCCCGGATGTGGGTGTGGGGGAGTCACAGGCAGAGGAGCCCAGAAGCTTTGAAGTCACAAGA
     spProGlyThrSerArgGlyProAspValGlyValGlyGluSerGlnAlaGluGluProArgSerPheGluValThrArg
 561 AGAGAAGGGCTTTCCAGCCACAACGAGCTGCTGGCCTCCTGCGGGAAGAAGTTCTGCAGCCGAGGGAGCCGGTGCGTGCT
     ArgGluGlyLeuSerSerHisAsnGluLeuLeuAlaSerCysGlyLysLysPheCysSerArgGlySerArgCysValLe
 641 CAGCAGGAAGACAGGGGAGCCCGAATGCCAGTGCCTGGAGGCATGCAGGCCCAGCTACGTGCCTGTGTGCGGCTCTGATG
     uSerArgLysThrGlyGluProGluCysGlnCysLeuGluAlaCysArgProSerTyrValProValCysGlySerAspG
 721 GGAGGTTTTATGAAAACCACTGTAAGCTCCACCGTGCTGCTTGCCTCCTGGGAAAGAGGATCACCGTCATCCACAGCAAG
     lyArgPheTyrGluAsnHisCysLysLeuHisArgAlaAlaCysLeuLeuGlyLysArgIleThrValIleHisSerLys
 801 GACTGTTTCCTCAAAGGTGACACGTGCACCATGGCCGGCTACGCCCGCTTGAAGAATGTCCTTCTGGCACTCCAGACCCG
     AspCysPheLeuLysGlyAspThrCysThrMetAlaGlyTyrAlaArgLeuLysAsnValLeuLeuAlaLeuGlnThrAr
 881 TCTGCAGCCACTCCAAGAAGGAGACAGCAGACAAGACCCTGCCTCCCAGAAGCGCCTCCTGGTGGAATCTCTGTTCAGGG
     gLeuGlnProLeuGlnGluGlyAspSerArgGlnAspProAlaSerGlnLysArgLeuLeuValGluSerLeuPheArgA
 961 ACTTAGATGCAGATGGCAATGGCCACCTCAGCAGCTCCGAACTGGCTCAGCATGTGCTGAAGAAGCAGGACCTGGATGAA
     spLeuAspAlaAspGlyAsnGlyHisLeuSerSerSerGluLeuAlaGlnHisValLeuLysLysGlnAspLeuAspGlu
1041 GACTTACTTGGTTGCTCACCAGGTGACCTCCTCCGATTTGACGATTACAACAGTGACAGCTCCCTGACCCTCCGCGAGTT
     AspLeuLeuGlyCysSerProGlyAspLeuLeuArgPheAspAspTyrAsnSerAspSerSerLeuThrLeuArgGluPh
1121 CTACATGGCCTTCCAAGTGGTTCAGCTCAGCCTCGCCCCCGAGGACAGGGTCAGTGTGACCACAGTGACCGTGGGGCTGA
     eTyrMetAlaPheGlnValValGlnLeuSerLeuAlaProGluAspArgValSerValThrThrValThrValGlyLeuS
1201 GCACAGTGCTGACCTGCGCCGTCCATGGAGACCTGAGGCCACCAATCATCTGGAAGCGCAACGGGCTCACCCTGAACTTC
     erThrValLeuThrCysAlaValHisGlyAspLeuArgProProIleIleTrpLysArgAsnGlyLeuThrLeuAsnPhe
1281 CTGGACTTGGAAGACATCAATGACTTTGGAGAGGATGATTCCCTGTACATCACCAAGGTGACCACCATCCACATGGGCAA
     LeuAspLeuGluAspIleAsnAspPheGlyGluAspAspSerLeuTyrIleThrLysValThrThrIleHisMetGlyAs
1361 TTACACCTGCCATGCTTCCGGCCACGAGCAGCTGTTCCAGACCCACGTCCTGCAGGTGAATGTGCCGCCAGTCATCCGTG
     nTyrThrCysHisAlaSerGlyHisGluGlnLeuPheGlnThrHisValLeuGlnValAsnValProProValIleArgV
1441 TCTATCCAGAGAGCCAGGCACAGGAGCCTGGAGTGGCAGCCAGCCTAAGATGCCATGCTGAGGGCATTCCCATGCCCAGA
     alTyrProGluSerGlnAlaGlnGluProGlyValAlaAlaSerLeuArgCysHisAlaGluGlyIleProMetProArg
1521 ATCACTTGGCTGAAAAACGGCGTGGATGTCTCAACTCAGATGTCCAAACAGCTCTCCCTTTTAGCCAATGGGAGCGAACT
     IleThrTrpLeuLysAsnGlyValAspValSerThrGlnMetSerLysGlnLeuSerLeuLeuAlaAsnGlySerGluLe
1601 CCACATCAGCAGTGTTCGGTATGAAGACACAGGGGCATACACCTGCATTGCCAAAAATGAAGTGGGTGTGGATGAAGATA
     uHisIleSerSerValArgTyrGluAspThrGlyAlaTyrThrCysIleAlaLysAsnGluValGlyValAspGluAspI
1681 TCTCCTCGCTCTTCATTGAAGACTCAGCTAGAAAGACCCTTGCAAACATCCTGTGGCGAGAGGAAGGCCTCAGCGTGGGA
     leSerSerLeuPheIleGluAspSerAlaArgLysThrLeuAlaAsnIleLeuTrpArgGluGluGlyLeuSerValGly
1761 AACATGTTCTATGTCTTCTCCGACGACGGTATCATCGTCATCCATCCTGTGGACTGTGAGATCCAGAGGCACCTCAAACC
     AsnMetPheTyrValPheSerAspAspGlyIleIleValIleHisProValAspCysGluIleGlnArgHisLeuLysPr
1841 CACGGAAAAGATTTTCATGAGCTATGAAGAAATCTGTCCTCAAAGAGAAAAAAATGCAACCCAGCCCTGCCAGTGGGTAT
     oThrGluLysIlePheMetSerTyrGluGluIleCysProGlnArgGluLysAsnAlaThrGlnProCysGlnTrpvalS
1921 CTGCAGTCAATGTCCGGAACCGGTACATCTATGTGGCCCAGCCAGCACTGAGCAGAGTCCTTGTGGTCGACATCCAAGCC
     erAlaValAsnValArgAsnArgTyrIleTyrValAlaGlnProAlaLeuSerArgValLeuValValAspIleGlnAla
2001 CAGAAAGTCCTACAGTCCATAGGTGTGGACCCTCTGCCGGCTAAGCTGTCCTATGACAAGTCACATGACCAAGTGTGGGT
     GlnLysValLeuGlnSerIleGlyValAspProLeuProAlaLysLeuSerTyrAspLysSerHisAspGlnValTrpVa
2081 CCTGAGCTGGGGGGACGTGCACAAGTCCCGACCAAGTCTCCAGGTGATCACAGAAGCCAGCACCGGCCAGAGCCAGCACC
     lLeuSerTrpGlyAspValHisLysSerArgProSerLeuGlnValIleThrGluAlaSerThrGlyGlnSerGlnHisL
2161 TCATCCGCACACCCTTTGCAGGAGTGGATGATTTCTTCATTCCCCCAACAAACCTCATCATCAACCACATCAGGTTTGGC
     euIleArgThrProPheAlaGlyValAspAspPhePheIleProProThrAsnLeuIleIleAsnHisIleArgPheGly
```

Fig. 8

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2241 TTCATCTTCAACAAGTCTGATCCTGCAGTCCACAAGGTGGACCTGGAAACAATGATGCCCCTCAAGACCATCGGCCTGCA
     PheIlePheAsnLysSerAspProAlaValHisLysValAspLeuGluThrMetMetProLeuLysThrIleGlyLeuHi
2321 CCACCATGGCTGCGTGCCCCAGGCCATGGCACACACCCACCTGGGCGGCTACTTCTTCATCCAGTGCCGACAGGACAGCC
     sHisHisGlyCysValProGlnAlaMetAlaHisThrHisLeuGlyGlyTyrPhePheIleGlnCysArgGlnAspSerP
2401 CCGCCTCTGCTGCCCGACAGCTGCTCGTTGACAGTGTCACAGACTCTGTGCTTGGCCCCAATGGTGATGTAACAGGCACC
     roAlaSerAlaAlaArgGlnLeuLeuValAspSerValThrAspSerValLeuGlyProAsnGlyAspValThrGlyThr
2481 CCACACACATCCCCCGACGGGCGCTTCATAGTCAGTGCTGCAGCTGACAGCCCCTGGCTGCACGTGCAGGAGATCACAGT
     ProHisThrSerProAspGlyArgPheIleValSerAlaAlaAlaAspSerProTrpLeuHisValGlnGluIleThrVa
2561 GCGGGGCGAGATCCAGACCCTGTATGACCTGCAAATAAACTCGGGCATCTCAGACTTGGCCTTCCAGCGCTCCTTCACTG
     lArgGlyGluIleGlnThrLeuTyrAspLeuGlnIleAsnSerGlyIleSerAspLeuAlaPheGlnArgSerPheThrG
2641 AAAGCAATCAATACAACATCTACGCGGCTCTGCACACGGAGCCGGACCTGCTGTTCCTGGAGCTGTCCACGGGGAAGGTG
     luSerAsnGlnTyrAsnIleTyrAlaAlaLeuHisThrGluProAspLeuLeuPheLeuGluLeuSerThrGlyLysVal
2721 GGCATGCTGAAGAACTTAAAGGAGCCACCCGCAGGGCCAGCTCAGCCCTGGGGGGTACCCACAGAATCATGAGGGACAG
     GlyMetLeuLysAsnLeuLysGluProProAlaGlyProAlaGlnProTrpGlyGlyThrHisArgIleMetArgAspSe
2801 TGGGCTGTTTGGACAGTACCTCCTCACACCAGCCCGAGAGTCACTGTTCCTCATCAATGGGAGACAAAACACGCTGCGGT
     rGlyLeuPheGlyGlnTyrLeuLeuThrProAlaArgGluSerLeuPheLeuIleAsnGlyArgGlnAsnThrLeuArgC
2881 GTGAGGTGTCAGGTATAAAGGGGGGGACCACAGTGGTGTGGGTGGGTGAGGTATGAAGGGCCCAGAGCAGAGCCCTGGGC
     ysGluValSerGlyIleLysGlyGlyThrThrValValTrpValGlyGluVal
2961 CAAGGAACACCCCCTAGTCCTGACACTGCAGCCTCAAGCAGGTACGCTGTACATTTTTACAGACAAAAGCAAAAACCTGT
3041 ACTCGCTTTGTGGTTCAACACTGGTCTCCTTGCAAGTTTCCTAGTATAAGGTATGCGCTGCTACCAAGATTGGGGTTTTT
3121 TCGTTAGGAAGTATGATTTATGCCTTGAGCTACGATGAGAACATATGCTGCTGTGTAAAGGGATCATTTCTGTGCCAAGC
3201 TGCACACCGAGTGACCTGGGGACATCATGGAACCAAGGGATCCTGCTCTCCAAGCAGACACCTCTGTCAGTTGCCTTCAC
3281 ATAGTCATTGTCCCTTACTGCCAGACCCAGCCAGACTTTGCCCTGACGGAGTGGCCCGGAAGCAGAGGCCGACCAGGAGC
3361 AGGGGCCTCCCTCCCGAACTGAAAGCCCATCCGTCCTCGCGTGGACCGCATCTTCTCCCTCGCAGCTGCTTCTTGCTTT
3441 TCTTTCCATTTGACTTGCTGTAAGCCTGAGGGAGAGCCAACAAGACTTACTGCATCTTGGGGGATGGGGAAATCACTCAC
3521 TTTATTTTGGAAATTTTTGATTAAAAAAAAATTTTATAATCTCAAATGCTAGTAAGCAGAAAGATGCTCTCCGAGGTCCA
3601 ACTATATCCTTCCCTGCCTTAGGCCGAGTCTCGGGGGTGGTCACAACCCCACATCCCACAGCCAGAAAGAACAATGGTCA
3681 TCTGAGAATACTGGCCCTGTCGACTATTGCCACCCTGCTTCTCCAAGAGCAGACCAGGCCACCTCATCCGTAAGGACTCG
3761 GTTCTGTGTTGGGACCCCAAAAAACCAGAACAAGTTCTGTGTGCCTCCTTTCAGCACAGAAGGGAGACATCTCATTAGTC
3841 AGGTCTGGTACCCCAGATTCAGGGCAGACTGGGCTTGCCTGGCAAGGTATGGGTGGCCTCCAGGCTCAATGCAGAAACCC
3921 CAAGGACACGAGTGGGGCCAGGTGAGTTCCTGAAGCTATACCTTTTCAAAACAGATTTTGTTTTCCTACCTGTGGCCCAT
4001 CCACTCCTCTCTGGTACCCCATCCCCGCATCAGCACTGCAGAGAGAACACATTTCGGCGAGGGTTTTCTTACCCACATTC
4081 CCCAATCAATACACACACACTGCAGAACCCAGAACAGAAGGCCACAGGCTGGCACTACTGCATTCTCCTTATGTGTCTCA
4161 GGCTGTGGTGACTCTCACATGGGCATCGAAGAAGTACAACCCACATAGCCCTCTGGAGACCGCCTAGATCAGAGACTCAG
4241 CAAAAACAGGCTCGCCTTCCCTCTCCCACATATGAGTGGAACTTACATGTGTCCTGGTTTGAATGATCATTTTGCAAGCC
4321 ACACGGGTTGGGAGAGGTGGTCTCACCACAGACGTCTTTGCTAATTTGGCCACCTTCACCTACTGACATGACCAGGATTT
4401 TCCTTTGCCATTAAGGAATGAACTCTTTCAAGGAGAGGAAACCCTAGACTCTGTGTCACTCTCAACACACACAGCTCCTT
4481 TCACTCCTGCCTGACTGCCAAGCCACCTGCATCCCCCGCCCCAGATCTCATGAGATCAATCACTTGTATGTCTCACGCAA
4561 CTTGGTCCACCAAACGCCTGTCCCCTGTAACTCCTAGGGGTGCGCCTAGACAGGTACGTCTGTTTTTTATTTTAAAAGAT
4641 ATGCTATGTAGATATAAGTTGAGGAAGCTCACCTCAAAAGCCTAGAATGCAGTTTCACAGTAGCTGGGATGCATGGATGA
4721 CCCATCTCACCCCTTTTTTTTTCCTGCCTCAATATCTTGATATGTTATGTTTACTCCCAATCTCCCATTTTTACCACTAA
4801 AATTCTCCAACTTTCATAAACTTTTTTTTGGAAAAATTTCCATTGTATCAGCCCCTGACAGAAAAAGGATCTCTGAGCCT
4881 AAAGGAGGAAAAGTCCCACCAACTACCAGACCAGAACACGAGCCCCTCTGGGCAGCAGGATTCCTAAGTCAAAGACCAGT
4961 TTGACCCAAACTGGCCTTTTAAAATAATCAGGAGTGACAGAGTCAACTTCTGCAGCACCTGCTTCTCCCCCACTGTCCCT
5041 TCCATCTTGGAATGTGTCTAAAAAAGCATAGCTGCCCTTTGCTGTCCTCAGAGTGCATTTCCTGGAGACGGCAGGCTTAG
5121 GTCTCACTGACAGCATGCCAGACACAACTGAATCGAAGCAGGCCTGAAGCCTAGGTCAGGGTTTCAGGAGTCCAGCCCCA
5201 GGAGGCAAAGTCACCAATGCAGGGAGGTAAATGCCTTTTGGCAGGAAAACCAATAGAGTTGGTTGGGTGGGGAGTCAGGG
5281 GTGGGAGGAGAAGGAGGAAGAGGAGGAAGGCCAGACTGGCCTGCCCTTTCTCCCATACTTCACCCCAGCAGAGGTTCATG
5361 GGACACAGTTGGAAAGCCACTGGGAGGAAATGCCTCACTACAGGGGGGCCTCCTGTAGCAAGCCCAGCCGGTAATCCTCC
5441 TAATGAACCCACAAGGTCAATTCACAACTGATATCTTAGCTATTAAAGAAGTACTGACTTTACCAAAAGAATCATCAAGA
5521 AAGCTATTTATATAAACCCCCTCAGTCATTTTGAAATAAAATTAATTTTACAA
```

Fig. 8 (continued)

FRAME: 3 - NUCLEOTIDE 420 TO 2864

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  1
   CAATTTCACACAGGAAACAGCTATGCCATGATTACGCAAGTTGGTACCGAGCTCGGATCCACTAGTAACGGCCGCCAGTG
 81
   TGCTGGAATTCGGCTTACTCACTATAGGGCTCGAGCGGCTGCCCGGGCAGGTCATTAATTCCATTTCTTTTTAGAGTATC
161
   ACAGCTTTCTCCTTCACTGACCACCCTTTGCTTCCTGTCAGAAAGCCCTGGACAGAACTCTCTGTGGGATTCTGCCCATG
241
   TTTCTGAGATATCGCCTCAATTGTCCTGGCTGGGCTGTCGGGTCTGCCCGTTTTACAGATGGGCAAACTGGAGTGGGAAG
321
   TATCCGGGTGGCTTCCTCAGGCCTGCAGCTGGTGGAGCAGCTACTGAAACAATCAGGAGCCCAGAAGCTTTGAAGTCACA
401
   AGAAGAGAAGACTCCCAGAATGCAGTGTGATGTTGGTGATGGACGCCTGTTTCGCCTTTCACTTAAACGTGCCCTTTCCA
                       MetGlnCysAspValGlyAspGlyArgLeuPheArgLeuSerLeuLysArgAlaLeuSerS
481
   GCTGCCCTGACCTCTTTGGGCTTTCCAGCCGCAACGAGCTGCTGGCCTCCTGCGGGAAGAAGTTCTGCAGCCGAGGGAGC
   erCysProAspLeuPheGlyLeuSerSerArgAsnGluLeuLeuAlaSerCysGlyLysLysPheCysSerArgGlySer
561
   CGGTGCGTGCTCAGCAGGAAGACAGGGGAGCCCGAATGCCAGTGCCTGGAGGCATGCAGGCCCAGCTACGTGCCTGTGTG
   ArgCysValLeuSerArgLysThrGlyGluProGluCysGlnCysLeuGluAlaCysArgProSerTyrValProValCy
641
   CGGCTCTGATGGGAGGTTTTATGAAAACCACTGTAAGCTCCACCGTGCTGCTTGCCTCCTGGGAAAGAGGATCACCGTCA
   sGlySerAspGlyArgPheTyrGluAsnHisCysLysLeuHisArgAlaAlaCysLeuLeuGlyLysArgIleThrValI
721
   TCCACAGCAAGGACTGTTTCCTCAAAGGTGACACGTGCACCATGGCCGGCTACGCCCGCTTGAAGAATGTCCTTCTGGCA
   leHisSerLysAspCysPheLeuLysGlyAspThrCysThrMetAlaGlyTyrAlaArgLeuLysAsnValLeuLeuAla
801
   CTCCAGACCCGTCTGCAGCCACTCCAAGAAGGAGACAGCAGACAAGACCCTGCCTCCCAGAAGCGCCTCCTGGTGGAATC
   LeuGlnThrArgLeuGlnProLeuGlnGluGlyAspSerArgGlnAspProAlaSerGlnLysArgLeuLeuValGluSe
881
   TCTGTTCAGGGACTTAGATGCAGATGGCAATGGCCACCTCAGCAGCTCCGAACTGGCTCAGCATGTGCTGAAGAAGCAGG
   rLeuPheArgAspLeuAspAlaAspGlyAsnGlyHisLeuSerSerSerGluLeuAlaGlnHisValLeuLysLysGlnA
961
   ACCTGGATGAAGACTTACTTGGTTGCTCACCAGGTGACCTCCTCCGATTTGACGATTACAACAGTGACAGCTCCCTGACC
   spLeuAspGluAspLeuLeuGlyCysSerProGlyAspLeuLeuArgPheAspAspTyrAsnSerAspSerSerLeuThr
1041
   CTCCGCGAGTTCTACATGGCCTTCCAAGTGGTTCAGCTCAGCCTCGCCCCCGAGGACAGGGTCAGTGTGACCACAGTGAC
   LeuArgGluPheTyrMetAlaPheGlnValValGlnLeuSerLeuAlaProGluAspArgValSerValThrThrValTh
1121
   CGTGGGGCTGAGCACAGTGCTGACCTGCGCCGTCCATGGAGACCTGAGGCCACCAATCATCTGGAAGCGCAACGGGCTCA
   rValGlyLeuSerThrValLeuThrCysAlaValHisGlyAspLeuArgProProIleIleTrpLysArgAsnGlyLeuT
1201
   CCCTGAACTTCCTGGACTTGGAAGACATCAATGACTTTGGAGAGGATGATTCCCTGTACATCACCAAGGTGACCACCATC
   hrLeuAsnPheLeuAspLeuGluAspIleAsnAspPheGlyGluAspAspSerLeuTyrIleThrLysValThrThrIle
1281
   CACATGGGCAATTACACCTGCCATGCTTCCGGCCACGAGCAGCTGTTCCAGACCCACGTCCTGCAGGTGAATGTGCCGCC
   HisMetGlyAsnTyrThrCysHisAlaSerGlyHisGluGlnLeuPheGlnThrHisValLeuGlnValAsnValProPr
```

Fig. 9

1361
AGTCATCCGTGTCTATCCAGAGAGCCAGGCACAGGAGCCTGGAGTGGCAGCCAGCCTAAGATGCCATGCTGAGGGCATTC
oValIleArgValTyrProGluSerGlnAlaGlnGluProGlyValAlaAlaSerLeuArgCysHisAlaGluGlyIleP
1441
CCATGCCCAGAATCACTTGGCTGAAAAACGGCGTGGATGTCTCAACTCAGATGTCCAAACAGCTCTCCCTTTTAGCCAAT
roMetProArgIleThrTrpLeuLysAsnGlyValAspValSerThrGlnMetSerLysGlnLeuSerLeuLeuAlaAsn
1521
GGGAGCGAACTCCACATCAGCAGTGTTCGGTATGAAGACACAGGGGCATACACCTGCATTGCCAAAAATGAAGTGGGTGT
GlySerGluLeuHisIleSerSerValArgTyrGluAspThrGlyAlaTyrThrCysIleAlaLysAsnGluValGlyVa
1601
GGATGAAGATATCTCCTCGCTCTTCATTGAAGACTCAGCTAGAAAGACCCTTGCAAACATCCTGTGGCGAGAGGAAGGCC
lAspGluAspIleSerSerLeuPheIleGluAspSerAlaArgLysThrLeuAlaAsnIleLeuTrpArgGluGluGlyL
1681
TCAGCGTGGGAAACATGTTCTATGTCTTCTCCGACGACGGTATCATCGTCATCCATCCTGTGGACTGTGAGATCCAGAGG
euSerValGlyAsnMetPheTyrValPheSerAspAspGlyIleIleValIleHisProValAspCysGluIleGlnArg
1761
CACCTCAAACCCACGGAAAAGATTTTCATGAGCTATGAAGAAATCTGTCCTCAAAGAGAAAAAAATGCAACCCAGCCCTG
HisLeuLysProThrGluLysIlePheMetSerTyrGluGluIleCysProGlnArgGluLysAsnAlaThrGlnProCy
1841
CCAGTGGGTATCTGCAGTCAATGTCCGGAACCGGTACATCTATGTGGCCCAGCCAGCACTGAGCAGAGTCCTTGTGGTCG
sGlnTrpValSerAlaValAsnValArgAsnArgTyrIleTyrValAlaGlnProAlaLeuSerArgValLeuValValA
1921
ACATCCAAGCCCAGAAAGTCCTACAGTCCATAGGTGTGGACCCTCTGCCGGCTAAGCTGTCCTATGACAAGTCACATGAC
spIleGlnAlaGlnLysvalLeuGlnSerIleGlyValAspProLeuProAlaLysLeuSerTyrAspLysSerHisAsp
2001
CAAGTGTGGGTCCTGAGCTGGGGGGACGTGCACAAGTCCCGACCAAGTCTCCAGGTGATCACAGAAGCCAGCACCGGCCA
GlnValTrpValLeuSerTrpGlyAspValHisLysSerArgProSerLeuGlnValIleThrGluAlaSerThrGlyGl
2081
GAGCCAGCACCTCATCCGCACACCCTTTGCAGGAGTGGATGATTTCTTCATTCCCCCAACAAACCTCATCATCAACCACA
nSerGlnHisLeuIleArgThrProPheAlaGlyValAspAspPhePheIleProProThrAsnLeuIleIleAsnHisI
2161
TCAGGTTTGGCTTCATCTTCAACAAGTCTGATCCTGCAGTCCACAAGGTGGACCTGGAAACAATGATGCCCCTCAAGACC
leArgPheGlyPheIlePheAsnLysSerAspProAlaValHisLysValAspLeuGluThrMetMetProLeuLysThr
2241
ATCGGCCTGCACCACCATGGCTGCGTGCCCCAGGCCATGGCACACACCCACCTGGGCGGCTACTTCTTCATCCAGTGCCG
IleGlyLeuHisHisHisGlyCysValProGlnAlaMetAlaHisThrHisLeuGlyGlyTyrPhePheIleGlnCysAr
2321
ACAGGACAGCCCCGCCTCTGCTGCCCGACAGCTGCTCGTTGACAGTGTCACAGACTCTGTGCTTGGCCCCAATGGTGATG
gGlnAspSerProAlaSerAlaAlaArgGlnLeuLeuValAspSerValThrAspSerValLeuGlyProAsnGlyAspV
2401
TAACAGGCACCCCACACACATCCCCCGACGGGCGCTTCATAGTCAGTGCTGCAGCTGACAGCCCCTGGCTGCACGTGCAG
alThrGlyThrProHisThrSerProAspGlyArgPheIleValSerAlaAlaAlaAspSerProTrpLeuHisValGln
2481
GAGATCACAGTGCGGGGCGAGATCCAGACCCTGTATGACCTGCAAATAAACTCGGGCATCTCAGACTTGGCCTTCCAGCG
GluIleThrValArgGlyGluIleGlnThrLeuTyrAspLeuGlnIleAsnSerGlyIleSerAspLeuAlaPheGlnAr
2561
CTCCTTCACTGAAAGCAATCAATACAACATCTACGCGGCTCTGCACACGGAGCCGGACCTGCTGTTCCTGGAGCTGTCCA
gSerPheThrGluSerAsnGlnTyrAsnIleTyrAlaAlaLeuHisThrGluProAspLeuLeuPheLeuGluLeuSerT

Fig. 9 (continued)

2641
CGGGGAAGGTGGGCATGCTGAAGAACTTAAAGGAGCCACCCGCAGGGCCAGCTCAGCCCTGGGGGGGTACCCACAGAATC
hrGlyLysValGlyMetLeuLysAsnLeuLysGluProProAlaGlyProAlaGlnProTrpGlyGlyThrHisArgIle
2721
ATGAGGGACAGTGGGCTGTTTGGACAGTACCTCCTCACACCAGCCCGAGAGTCACTGTTCCTCATCAATGGGAGACAAAA
MetArgAspSerGlyLeuPheGlyGlnTyrLeuLeuThrProAlaArgGluSerLeuPheLeuIleAsnGlyArgGlnAs
2801
CACGCTGCGGTGTGAGGTGTCAGGTATAAAGGGGGGGACCACAGTGGTGTGGGTGGGTGAGGTATGAAGGGCCCAGAGCA
nThrLeuArgCysGluValSerGlyIleLysGlyGlyThrThrValValTrpValGlyGluVal
2881
GAGCCCTGGGCCAAGGAACACCCCCTAGTCCTGACACTGCAGCCTCAAGCAGGTACGCTGTACATTTTTACAGACAAAAG
2961
CAAAAACCTGTACTCGCTTTGTGGTTCAACACTGGTCTCCTTGCAAGTTTCCTAGTATAAGGTATGCGCTGCTACCAAGA
3041
TTGGGGTTTTTTCGTTAGGAAGTATGATTTATGCCTTGAGCTACGATGAGAACATATGCTGCTGTGTAAAGGGATCATTT
3121
CTGTGCCAAGCTGCACACCGAGTGACCTGGGGACATCATGGAACCAAGGGATCCTGCTCTCCAAGCAGACACCTCTGTCA
3201
GTTGCCTTCACATAGTCATTGTCCCTTACTGCCAGACCCAGCCAGACTTTGCCCTGACGGAGTGGCCCGGAAGCAGAGGC
3281
CGACCAGGAGCAGGGGCCTCCCTCCCGAACTGAAAGCCCATCCGTCCTCGCGTGGGACCGCATCTTCTCCCTCGCAGCTG
3361
CTTCTTGCTTTTCTTTCCATTTGACTTGCTGTAAGCCTGAGGGAGAGCCAACAAGACTTACTGCATCTTGGGGGATGGGG
3441
AAATCACTCACTTTATTTTGGAAATTTTTGATTAAAAAAAAATTTTATAATCTCAAATGCTAGTAAGCAGAAAGATGCTC
3521
TCCGAGGTCCAACTATATCCTTCCCTGCCTTAGGCCGAGTCTCGGGGGTGGTCACAACCCCACATCCCACAGCCAGAAAG
3601
AACAATGGTCATCTGAGAATACTGGCCCTGTCGACTATTGCCACCCTGCTTCTCCAAGAGCAGACCAGGCCACCTCATCC
3681
GTAAGGACTCGGTTCTGTGTTGGACCCCAAAAAACCAGAACAAGTTCTGTGTGCCTCCTTTCAGCACAGAAGGGAGACA
3761
TCTCATTAGTCAGGTCTGGTACCCCAGATTCAGGGCAGACTGGGCTTGCCTGGCAAGGTATGGGTGGCCTCCAGGCTCAA
3841
TGCAGAAACCCCAAGGACACGAGTGGGGCCAGGTGAGTTCCTGAAGCTATACCTTTTCAAAACAGATTTTGTTTTCCTAC
3921
CTGTGGCCCATCCACTCCTCTCTGGTACCCCATCCCCGCATCAGCACTGCAGAGAGAACACATTTCGGCGAGGGTTTTCT
4001
TACCCACATTCCCCAATCAATACACACACACTGCAGAACCCAGAACAGAAGGCCACAGGCTGGCACTACTGCATTCTCCT
4081
TATGTGTCTCAGGCTGTGGTGACTCTCACATGGGCATCGAAGAAGTACAACCCACATAGCCCTCTGGAGACCGCCTAGAT
4161
CAGAGACTCAGCAAAAACAGGCTCGCCTTCCCTCTCCCACATATGAGTGGAACTTACATGTGTCCTGGTTTGAATGATCA
4241
TTTTGCAAGCCACACGGGTTGGGAGAGGTGGTCTCACCACAGACGTCTTTGCTAATTTGGCCACCTTCACCTACTGACAT
4321
GACCAGGATTTTCCTTTGCCATTAAGGAATGAACTCTTTCAAGGAGAGGAAACCCTAGACTCTGTGTCACTCTCAACACA
4401
CACAGCTCCTTTCACTCCTGCCTGACTGCCAAGCCACCTGCATCCCCCGCCCCAGATCTCATGAGATCAATCACTTGTAT

Fig. 9 (continued)

4481
GTCTCACGCAACTTGGTCCACCAzACGCCTGTCCCCTGTAACTCCTAGGGGTGCGCCTAGACAGGTACGTCTGTTTTTTA
4561
TTTTAAAAGATATGCTATGTAGATATAAGTTGAGGAAGCTCACCTCAAAAGCCTAGAATGCAGTTTCACAGTAGCTGGGA
4641
TGCATGGATGACCCATCTCACCCCTTTTTTTTTCCTGCCTCAATATCTTGATATGTTATGTTTACTCCCAATCTCCCATT
4721
TTTACCACTAAAATTCTCCAACTTTCATAAACTTTTTTTTGGAAAAATTTCCATTGTATCAGCCCCTGACAGARAAAGGA
4801
TCTCTGAGCCTAAAGGAGGAAAAGTCCCACCAACTACCAGACCAGAACACGAGCCCCTCTGGGCAGCAGGATTCCTAAGT
4881
CAAAGACCAGTTTGACCCAAACTGGCCTTTTAAAATAATCAGGAGTGACAGAGTCAACTTCTGCAGCACCTGCTTCTCCC
4961
CCACTGTCCCTTCCATCTTGGAATGTGTCTAAAAAAGCATAGCTGCCCTTTGCTGTCCTCAGAGTGCATTTCCTGGAGAC
5041
GGCAGGCTTAGGTCTCACTGACAGCATGCCAGACACAACTGAATCGAAGCAGGCCTGAAGCCTAGGTCAGGGTTTCAGGA
5121
GTCCAGCCCCAGGAGGCAAAGTCACCAATGCAGGGAGGTAAATGCCTTTTGGCAGGAAAACCAATAGAGTTGGTTGGGTG
5201
GGGAGTCAGGGGTGGGAGGAGAAGGAGGAAGAGGAGGAAGGCCAGACTGGCCTGCCCTTTCTCCCATACTTCACCCCAGC
5281
AGAGGTTCATGGGACACAGTTGGAAAGCCACTGGGAGGAAATGCCTCACTACAGGGGGGCCTCCTGTAGCAAGCCCAGCC
5361
GGTAATCCTCCTAATGAACCCACAAGGTCAATTCACAACTGATATCTTAGCTATTAAAGAAGTACTGACTTTACCARAAG
5441
AATCATCAAGAAAGCTATTTATATAAACCCCCTCAGTCATTTTGAAATAAAATTAATTTTAC

Fig. 9 (continued)

TRANSLATED PROTEIN - NUCLEOTIDE 124 TO 1089

```
  1 CTTTGCTTCAGCCGCAGTCGCCACTGGCTGCCTGAGGTGCTCTTA
 46 CAGCCTGTTCCAAGTGTGGCTTAATCCGTCTCCACCACCAGATCT

 91 TTCTCCGTGGATTCCTCTGCTAAGACCGCTGCCATGCCAGTGACG
                                        MetProValThr

136 GTAACCCGCACCACCATCACAACCACCACGACGTCATCTTCGGGC
    ValThrArgThrThrIleThrThrThrThrThrSerSerSerGly

181 CTGGGGTCCCCCATGATCGTGGGGTCCCCTCGGGCCCTGACACAG
    LeuGlySerProMetIleValGlySerProArgAlaLeuThrGln

226 CCCCTGGGTCTCCTTCGCCTGCTGCAGCTGGTGTCTACCTGCGTG
    ProLeuGlyLeuLeuArgLeuLeuGlnLeuValSerThrCysVal

271 GCCTTCTCGCTGGTGGCTAGCGTGGGCGCCTGGACGGGGTCCATG
    AlaPheSerLeuValAlaSerValGlyAlaTrpThrGlySerMet

316 GGCAACTGGTCCATGTTCACCTGGTGCTTCTGCTTCTCCGTGACC
    GlyAsnTrpSerMetPheThrTrpCysPheCysPheSerValThr

361 CTGATCATCCTCATCGTGGAGCTGTGCGGGCTCCAGGCCCGCTTC
    LeuIleIleLeuIleValGluLeuCysGlyLeuGlnAlaArgPhe

406 CCCCTGTCTTGGCGCAACTTCCCCATCACCTTCGCCTGCTATGCG
    ProLeuSerTrpArgAsnPheProIleThrPheAlaCysTyrAla

451 GCCCTCTTCTGCCTCTCGGCCTCCATCATCTACCCCACCACCTAT
    AlaLeuPheCysLeuSerAlaSerIleIleTyrProThrThrTyr

496 GTCCAGTTCCTGTCCCACGGCCGTTCGCGGGACCACGCCATCGCC
    ValGlnPheLeuSerHisGlyArgSerArgAspHisAlaIleAla

541 GCCACCTTCTTCTCCTGCATCGCGTGTGTGGCTTACGCCACCGAA
    AlaThrPhePheSerCysIleAlaCysValAlaTyrAlaThrGlu

586 GTGGCCTGGACCCGGGCCCGGCCCGGCGAGATCACTGGCTATATG
    ValAlaTrpThrArgAlaArgProGlyGluIleThrGlyTyrMet

631 GCCACCGTACCCGGGCTGCTGAAGGTGCTGGAGACCTTCGTTGCC
    AlaThrValProGlyLeuLeuLysValLeuGluThrPheValAla

676 TGCATCATCTTCGCGTTCATCAGCGACCCCAACCTGTACCAGCAC
    CysIleIlePheAlaPheIleSerAspProAsnLeuTyrGlnHis
```

Fig. 10

721 CAGCCGGCCCTGGAGTGGTGCGTGGCGGTGTACGCCATCTGCTTC
GlnProAlaLeuGluTrpCysValAlaValTyrAlaIleCysPhe

766 ATCCTAGCGGCCATCGCCATCCTGCTGAACCTGGGGGAGTGCACC
IleLeuAlaAlaIleAlaIleLeuLeuAsnLeuGlyGluCysThr

811 AACGTGCTACCCATCCCCTTCCCCAGCTTCCTGTCGGGGCTGGCC
AsnValLeuProIleProPheProSerPheLeuSerGlyLeuAla

856 TTGCTGTCTGTCCTCCTCTATGCCACCGCCCTTGTTCTCTGGCCC
LeuLeuSerValLeuLeuTyrAlaThrAlaLeuValLeuTrpPro

901 CTCTACCAGTTCGATGAGAAGTATGGCGGCCAGCCTCGGCGCTCG
LeuTyrGlnPheAspGluLysTyrGlyGlyGlnProArgArgSer

946 AGAGATGTAAGCTGCAGCCGCAGCCATGCCTACTACGTGTGTGCC
ArgAspValSerCysSerArgSerHisAlaTyrTyrValCysAla

991 TGGGACCGCCGACTGGCTGTGGCCATCCTGACGGCCATCAACCTA
TrpAspArgArgLeuAlaValAlaIleLeuThrAlaIleAsnLeu

1036 CTGGCGTATGTGGCTGACCTGGTGCACTCTGCCCACCTGGTTTTT
LeuAlaTyrValAlaAspLeuValHisSerAlaHisLeuValPhe

1081 GTCAAGGTCTAAGACTCTCCCAAGAGGCTCCCGTTCCCTCTCCAA
ValLysVal

1126 CCTCTTTGTTCTTCTTGCCCGAGTTTTCTTTATGGAGTACTTCTT

1171 TCCTCCGCCTTTCCTCTGTTTTCCTCTTCCTGTCTCCC

Fig. 10 (continued)

TRANSLATED PROTEIN - NUCLEOTIDE 587 TO 1012

```
   1 GGAAGAAGAAGGAGGAGGAGGAGAAGGAGAAGAAGAAGGAGAAGA
  46 ACGCAAGACTTCGTCTCAAAAAAAAAGAAGAAAAAATTTAAATAC
  91 ATTTAAAAAAGAAGGTTGCATGCTGTGGAGCAACCAGACAATTGT
 136 GATGAAATGTGAAGCACAAGGCACCAGCTGTGACGTGTTTTTGCC
 181 AAGAAGTCAAACCACGTTCCAACTAAACCTCTAGAGCAAACTTTC
 226 ATTTTCAGCAAATTCGAAGAAAAGAGGAATAATGTAAATGACCCC
 271 ACAGGGAAACAGACAAACCCTGAATGTGGAGCATTTCACAGGACA
 316 AAACCTGGACAGACATCGGAACACTTACAGGATGTGTGTAGTGTG
 361 GCATGACAGAGAACTTTGGTTTCCTTTAATGTGACTGTAGACCTG
 406 GCAGTGTTACTATAAGAATCACTGGCAATCAGACACCCGGGTGTG
 451 CTGAGCTGGCACTCAGTGGGGGCGGCTACTGCTCATGTGATTGTG
 496 GAGTAGACAGTTGGAAGAAGTACCCAGTCCATTTGGAGAGTTAAA
 541 ACTGTGCCTAACAGAGGTGTCCTCTGACTTTTCTTCTGCAAGCTC

 586 CATGTTTTCACATCTTCCCTTTGACTGTGTCCTGCTGCTGCTGCT
      MetPheSerHisLeuProPheAspCysValLeuLeuLeuLeuLe

 631 GCTACTACTTACAAGGTCCTCAGAAGTGGAATACAGAGCGGAGGT
     uLeuLeuLeuThrArgSerSerGluValGluTyrArgAlaGluVa

 676 CGGTCAGAATGCCTATCTGCCCTGCTTCTACACCCCAGCCGCCCC
     lGlyGlnAsnAlaTyrLeuProCysPheTyrThrProAlaAlaPr

 721 AGGGAACCTCGTGCCCGTCTGCTGGGGCAAAGGAGCCTGTCCTGT
     oGlyAsnLeuValProValCysTrpGlyLysGlyAlaCysProVa

 766 GTTTGAATGTGGCAACGTGGTGCTCAGGACTGATGAAAGGGATGT
     lPheGluCysGlyAsnValValLeuArgThrAspGluArgAspVa

 811 GAATTATTGGACATCCAGATACTGGCTAAATGGGGATTTCCGCAA
     lAsnTyrTrpThrSerArgTyrTrpLeuAsnGlyAspPheArgLy

 856 AGGAGATGTGTCCCTGACCATAGAGAATGTGACTCTAGCAGACAG
     sGlyAspValSerLeuThrIleGluAsnValThrLeuAlaAspSe

 901 TGGGATCTACTGCTGCCGGATCCAAATCCCAGGCATAATGAATGA
     rGlyIleTyrCysCysArgIleGlnIleProGlyIleMetAsnAs

 946 TGAAAAATTTAACCTGAAGTTGGTCATCAAACCAGGTGAGTGGAC
     pGluLysPheAsnLeuLysLeuValIleLysProGlyGluTrpTh

 991 ATTTGCATGCCATCTTTATGAATAAGATTTATCTGTGGATCATAT
     rPheAlaCysHisLeuTyrGlu

1036 TAAAGGTACTGATTGTTCTCATCTCTGACTTCCCTAATTATAGCC
1081 CTGGAGGAGGGCCACTAAGACCTAAAGTTTAACAGGCCCCATTGG
1126 TGATGCTCAGTGATATTTAACACCTTCTCTCTGTTTTAAAACTCA
1171 TGGGTGTGCCTGGGCGTGGTGGCTCACACCTCT
```

Fig. 11

TRANSLATED PROTEIN - NUCLEOTIDE 494 TO 769

1 TCTAGAACATTCTCCAGCCCTTTTTTTCTTTTGCTCTTTTATGAC
46 ATTGACATGAAGAGTCCGGGCCAGTTGTTCTGGATTTGTCTGATT
91 GCTTCTCCCTGGTTGGAGTCAGGTGGAACAGCTCTGGCAGGAACG
136 CCCCCCCGGGCAATGCAGAGTCCTCCTCCAGGAGGCACTTAGTGT
181 CCATGCGTCACCTTGCTGGTGATGCTTCACTGGATCACTTGGTTC
226 CGGGGTTGTCCGCACGTCTCCCTGTAGTGCAGGTGCTCCTTCCTC
271 TTTCCAATTAGCCTGTGGGATGGGACTTGGAAGCTGTGTCTGTTC
316 TGCTCCACTGGCAACCTTTTCTTCAATGACTTAAGCTGGTGTTTT
361 GCCATTTTCCATACTCTATCATGGGGAGTGTTCAGTATCGGCATC
406 TAGAGATCTCCCCTGGCCCCATCACAGCTAGAGCTATGCTGTCCC

451 CTTTCAGGGACATCTTGTAATTTATCCACCCAGCCCCCAACTGAT
Me

496 GGACATAAAGGCTGTCTCCCCATCATCTCCTGCTACTACAGACAG
tAspIleLysAlaValSerProSerSerProAlaThrThrAspSe

541 CACTGCAGGGACTGTCCTGCTGTGTTTTTTAAGGCATGGGTACT
rThrAlaGlyThrValLeuLeuCysPhePheLysAlaTrpValLe

586 CCAGAAGCAGTTGCTCAGCTGCACCCCCAAGGTTGAGTGGAAGTC
uGlnLysGlnLeuLeuSerCysThrProLysValGluTrpLysSe

631 CCTCGGTAAAGGAGGAGGAGAGAGTGTGAAGGGAATGGCAAGGCG
rLeuGlyLysGlyGlyGlyGluSerValLysGlyMetAlaArgAr

676 GGGAGGGAGACAGGGCACAGGTGTCCTGGCAACAGCAGATGGGAA
gGlyGlyArgGlnGlyThrGlyValLeuAlaThrAlaAspGlyLy

721 ACAGGTCTGGCTAAGGTACCAGAAGCCAACAAGTCCCAGAAAGGT
sGlnValTrpLeuArgTyrGlnLysProThrSerProArgLysVa

766 CAAGTGACTTTCCCAAGGTCACACAGCAAGTTGATGGCAGAGCTG
lLys

811 GGTACAGGACTCAGA

Fig. 12

TRANSLATED PROTEIN - NUCLEOTIDE 83 TO 889

```
  1 CTAGAATTCAGCGGCCGCTGAATTCTAGTGCAGAGTGAGCAAGGG

 46 CCGCCTCATCCAGCTTCTCTCTGAGAGCCAGGGCCACATGGCTCA
                                           MetAlaHi

 91 CCTGGTGAACTCCGTCAGCGACATCCTGGATGCCCTGCAGAGGGA
    sLeuValAsnSerValSerAspIleLeuAspAlaLeuGlnArgAs

136 CCGGGGGCTGGGCCGGCCCCGCAACAAGGCCGACCTTCAGAGAGC
    pArgGlyLeuGlyArgProArgAsnLysAlaAspLeuGlnArgAl

181 GCCTGCCCGGGGAACCCGGCCCCGGGGCTGTGCCACTGGCTCCCG
    aProAlaArgGlyThrArgProArgGlyCysAlaThrGlySerAr

226 GCCCCGAGACTGTCTGGACGTCCTCCTAAGCGGACAGCAGGACGA
    gProArgAspCysLeuAspValLeuLeuSerGlyGlnGlnAspAs

271 TGGCGTCTACTCTGTCTTTCCCACCCACTACCCGGCCGGCTTCCA
    pGlyValTyrSerValPheProThrHisTyrProAlaGlyPheGl

316 GGTGTACTGTGACATGCGCACGGACGGCGGCGGCTGGACGGTGTT
    nValTyrCysAspMetArgThrAspGlyGlyGlyTrpThrValPh

361 TCAGCGCCGGGAGGACGGCTCCGTGAACTTCTTCCGGGGCTGGGA
    eGlnArgArgGluAspGlySerValAsnPhePheArgGlyTrpAs

406 TGCGTACCGAGACGGCTTTGGCAGGCTCACCGGGGAGCACTGGCT
    pAlaTyrArgAspGlyPheGlyArgLeuThrGlyGluHisTrpLe

451 AGGGCTCAAGAGGATCCACGCCCTGACCACACAGGCTGCCTACGA
    uGlyLeuLysArgIleHisAlaLeuThrThrGlnAlaAlaTyrGl

496 GCTGCACGTGGACCTGGAGGACTTTGAGAATGGCACGGCCTATGC
    uLeuHisValAspLeuGluAspPheGluAsnGlyThrAlaTyrAl

541 CCGCTACGGGAGCTTCGGCGTGGGCTTGTTCTCCGTGGACCCTGA
    aArgTyrGlySerPheGlyValGlyLeuPheSerValAspProGl

586 GGAAGACGGGTACCCGCTCACCGTGGCTGACTATTCCGGCACTGC
    uGluAspGlyTyrProLeuThrValAlaAspTyrSerGlyThrAl

631 AGGCGACTCCCTCCTGAAGCACAGCGGCATGAGGTTCACCACCAA
    aGlyAspSerLeuLeuLysHisSerGlyMetArgPheThrThrLy

676 GGACCGTGACAGCGACCATTCAGAGAACAACTGTGCCGCCTTCTA
    sAspArgAspSerAspHisSerGluAsnAsnCysAlaAlaPheTy
```

Fig. 13

```
721  CCGCGGTGCCTGGTGGTACCGCAACTGCCACACGTCCAACCTCAA
     rArgGlyAlaTrpTrpTyrArgAsnCysHisThrSerAsnLeuAs

766  TGGGCAGTACCTGCGCGGTGCGCACGCCTCCTATGCCGACGGCGT
     nGlyGlnTyrLeuArgGlyAlaHisAlaSerTyrAlaAspGlyVa

811  GGAGTGGTCCTCCTGGACCGGCTGGCAGTACTCACTCAAGTTCTC
     lGluTrpSerSerTrpThrGlyTrpGlnTyrSerLeuLysPheSe

856  TGAGATGAAGATCCGGCCGGTCCGGGAGGACCGCTAGACCGGTGC
     rGluMetLysIleArgProValArgGluAspArg

901  ACCTTGTCCTTGGCCCTGCTGGTCCCTGTCGCCCCATCCCCGACC

946  CCACCTCACTCTTTCGTGAATGTTCTCCACCCACCTGTGCCTGGC

991  GGACCCACTCTCCAGTAGGGAGGGGCCGGGCCATCCCTGACACGA

1036 AGCTCCCTGGGCCGGTGAAGTCACACATCGCCTTCTCGCCGTCCC

1081 CACCCCCTCCATTTGGCAG
```

Fig. 13 (continued)

TRANSLATED PROTEIN - FRAME: 2 - NUCLEOTIDE 38 TO 844

```
 1
  CCGCCTCATCCAGCTTCTCTCTGAGAGCCAGGGCCACATGGCTCA
                                       MetAlaHi
 46
  CCTGGTGAACTCCGTCAGCGACATCCTGGATGCCCTGCAGAGGGA
  sLeuValAsnSerValSerAspIleLeuAspAlaLeuGlnArgAs
 91
  CCGGGGGCTGGGCCGGCCCCGCAACAAGGCCGACCTTCAGAGAGC
  pArgGlyLeuGlyArgProArgAsnLysAlaAspLeuGlnArgAl
136
  GCCTGCCCGGGGAACCCGGCCCCGGGGCTGTGCCACTGGCTCCCG
  aProAlaArgGlyThrArgProArgGlyCysAlaThrGlySerAr
181
  GCCCCGAGACTGTCTGGACGTCCTCCTAAGCGGACAGCAGGACGA
  gProArgAspCysLeuAspValLeuLeuSerGlyGlnGlnAspAs
226
  TGGCGTCTACTCTGTCTTTCCCACCCACTACCCGGCCGGCTTCCA
  pGlyValTyrSerValPheProThrHisTyrProAlaGlyPheGl
271
  GGTGTACTGTGACATGCGCACGGACGGCGGCGGCTGGACGGTGTT
  nValTyrCysAspMetArgThrAspGlyGlyGlyTrpThrValPh
316
  TCAGCGCCGGGAGGACGGCTCCGTGAACTTCTTCCGGGGCTGGGA
  eGlnArgArgGluAspGlySerValAsnPhePheArgGlyTrpAs
361
  TGCGTACCGAGACGGCTTTGGCAGGCTCACCGGGGAGCACTGGCT
  pAlaTyrArgAspGlyPheGlyArgLeuThrGlyGluHisTrpLe
406
  AGGGCTCAAGAGGATCCACGCCCTGACCACACAGGCTGCCTACGA
  uGlyLeuLysArgIleHisAlaLeuThrThrGlnAlaAlaTyrGl
451
  GCTGCACGTGGACCTGGAGGACTTTGAGAATGGCACGGCCTATGC
  uLeuHisValAspLeuGluAspPheGluAsnGlyThrAlaTyrAl
496
  CCGCTACGGGAGCTTCGGCGTGGGCTTGTTCGCCGTGGACCCTGA
  aArgTyrGlySerPheGlyValGlyLeuPheAlaValAspProGl
541
  GGAAGACGGGCACCCGCTCACCGTGGCTGACTATTCCGGCACTGC
  uGluAspGlyHisProLeuThrValAlaAspTyrSerGlyThrAl
586
  AGGCGACTCCCTCCTGAAGCACAGCGGCATGAGGTTCACCACCAA
  aGlyAspSerLeuLeuLysHisSerGlyMetArgPheThrThrLy
631
  GGACCGTGACAGCGACCATTCAGAGAACAACTGTGCCGCCTTCTA
  sAspArgAspSerAspHisSerGluAsnAsnCysAlaAlaPheTy
```

Fig. 14

676
CCGCGGTGCCTGGTGGTACCGCAACTGCCACACGTCCAACCTCAA
rArgGlyAlaTrpTrpTyrArgAsnCysHisThrSerAsnLeuAs
721
TGGGCAGTACCTGCGCGGTGCGCACGCCTCCTATGCCGACGGCGT
nGlyGlnTyrLeuArgGlyAlaHisAlaSerTyrAlaAspGlyVa
766
GGAGTGGTCCTCCTGGACCGGCTGGCAGTACTCACTCAAGTTCTC
lGluTrpSerSerTrpThrGlyTrpGlnTyrSerLeuLysPheSe
811
TGAGATGAAGATCCGGCCGGTCCGGGAGGACCGCTAGACCGGTGC
rGluMetLysIleArgProValArgGluAspArg
856
ACCTTGTCCTTGGCCCTGCTGGTCCCTGTCGCCCCATCCCCGACC
901
CCACCTCACTCTTTCGTGAATGTTCTCCACCCACCTGTGCCTGGC
946
GGACCCACTCTCCAGTAGGGAGGGGCCGGGCCATCCCTGACACGA
991
AGCTCCCTGGGCCGGTGAAGTCACACATCGCCTTCTCGCCGTCCC
1036
CACCCCCTCCATTTGGCAG

Fig. 14 (continued)

Fig. 15

Fig. 16

Fig. 17

FRAME: 1 - NUCLEOTIDE 1 TO 498

1
ATGAATTTTCTGAAATTAATTGCTGTGTTTATAGTTTTTAGCCAT
MetAsnPheLeuLysLeuIleAlaValPheIleValPheSerHis
46
GCATCGGAATCACCTCAGGACTCCACTCCCAATCAATTATATATC
AlaSerGluSerProGlnAspSerThrProAsnGlnLeuTyrIle
91
TGGGGGAGGACCAAGGCGTTGGTATTTTTCAGAAGCTCCACTGGT
TrpGlyArgThrLysAlaLeuValPhePheArgSerSerThrGly
136
GATTCTGACAGCACAGCTAGGATTAAGAAACTGATCAATGGGAAC
AspSerAspSerThrAlaArgIleLysLysLeuIleAsnGlyAsn
181
AGCATGCCTGTTGCAGAGGAGCTTCCCTGGGAAATGTCACACACA
SerMetProValAlaGluGluLeuProTrpGluMetSerHisThr
226
GAACATCAATCTTCCTTCCCCACTCCTGAGATCCCTCATTCTTTG
GluHisGlnSerSerPheProThrProGluIleProHisSerLeu
271
GCACCAGGAACAGTTGCAATTAGTAAACCCTGGTTCCCTGCTGTC
AlaProGlyThrValAlaIleSerLysProTrpPheProAlaVal
316
TCACAAATCGCAAGAGTCCAACGTGTGGATATAAACTTTTGTTCA
SerGlnIleAlaArgValGlnArgValAspIleAsnPheCysSer
361
TGGGAGGATCTTTCTCCCAGTGGAAAAGCAACTGGGAAAAGCAGG
TrpGluAspLeuSerProSerGlyLysAlaThrGlyLysSerArg
406
ACACACTGCACAGTGACTGCAGTTTCATCCAATGCCACCACCCAT
ThrHisCysThrValThrAlaValSerSerAsnAlaThrThrHis
451
GCAGGCATAAATAATGAACATGGATGGGGGAGTCTGGAGCTGCTG
AlaGlyIleAsnAsnGluHisGlyTrpGlySerLeuGluLeuLeu
496
AAT
Asn

Fig. 18

CAGAGAGCGCCTGCCCGGGGAACCCGGCCCCGGGGCTGTGCCACTGGCTCCCGGCCCCGAGACTGTCTGGACGTCCT
CCTAAGCGGACAGCAGGACGATGGCGTCTACTCTGTCTTTCCCACCCACTACCCGGCCGGCTTCCAGGTGTACTGTG
ACATGCGCACGGACGGCGGCGGCTGGACGGTGTTTCAGCGCCGGGAGGACGGCTCCGTGAACTTCTTCCGGGGCTGG
GACGCGTACCGAGACGGCTTTGGCAGGCTCACCGGGGAGCACTGGCTAGGGCTCAAGAGGATCCACGCCCTGACCAC
ACAGGCTGCCTACGAGCTGCACGTGGACCTGGAGGACTTTGAGAATGGCACGGCCTATGCCCGCTACGGGAGCTTCG
GCGTGGGCTTGTTCGCCGTGGACCCTGAGGAAGACGGGTACCCGCTCACCGTGGCTGACTATTCCGGCACTGCAGGC
GACTCCCTCCTGAAGCACAGCGGCATGAGGTTCACCACCAAGGACCGTGACAGCGACCATTCAGAGAACAACTGTGC
CGCCTTCTACCGCGGTGCCTGGTGGTACCGCAACTGCCACACGTCCAACCTCAATGGGCAGTACCTGCGCGGTGCGC
ACGCCTCCTATGCCGACGGCGTGGAGTGGTCCTCCTGGACCGGCTGGCAGTACTCACTCAAGTTCTCTGAGATGAAG
ATCCGGCCGGTCCGG GAGGACCGC

Fig. 19

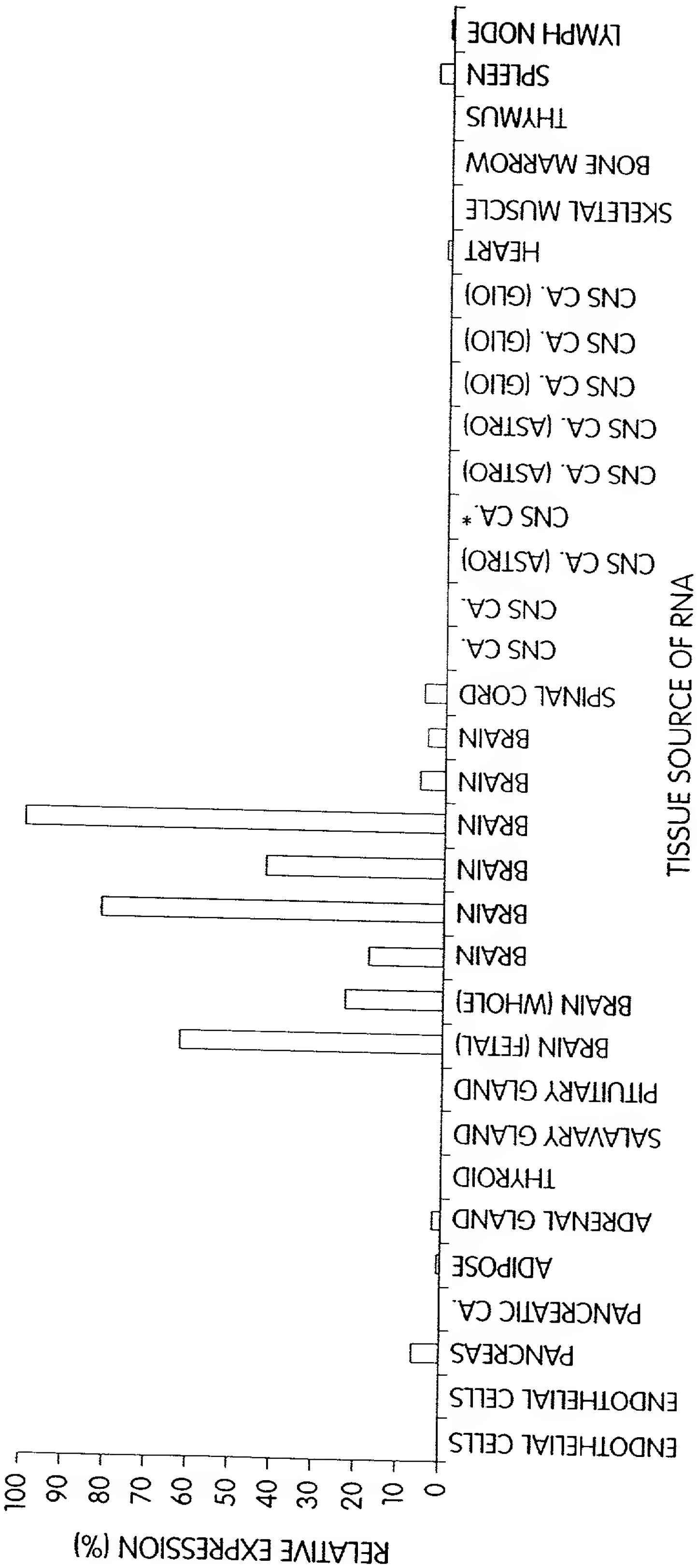

Fig. 20 (PANEL A)

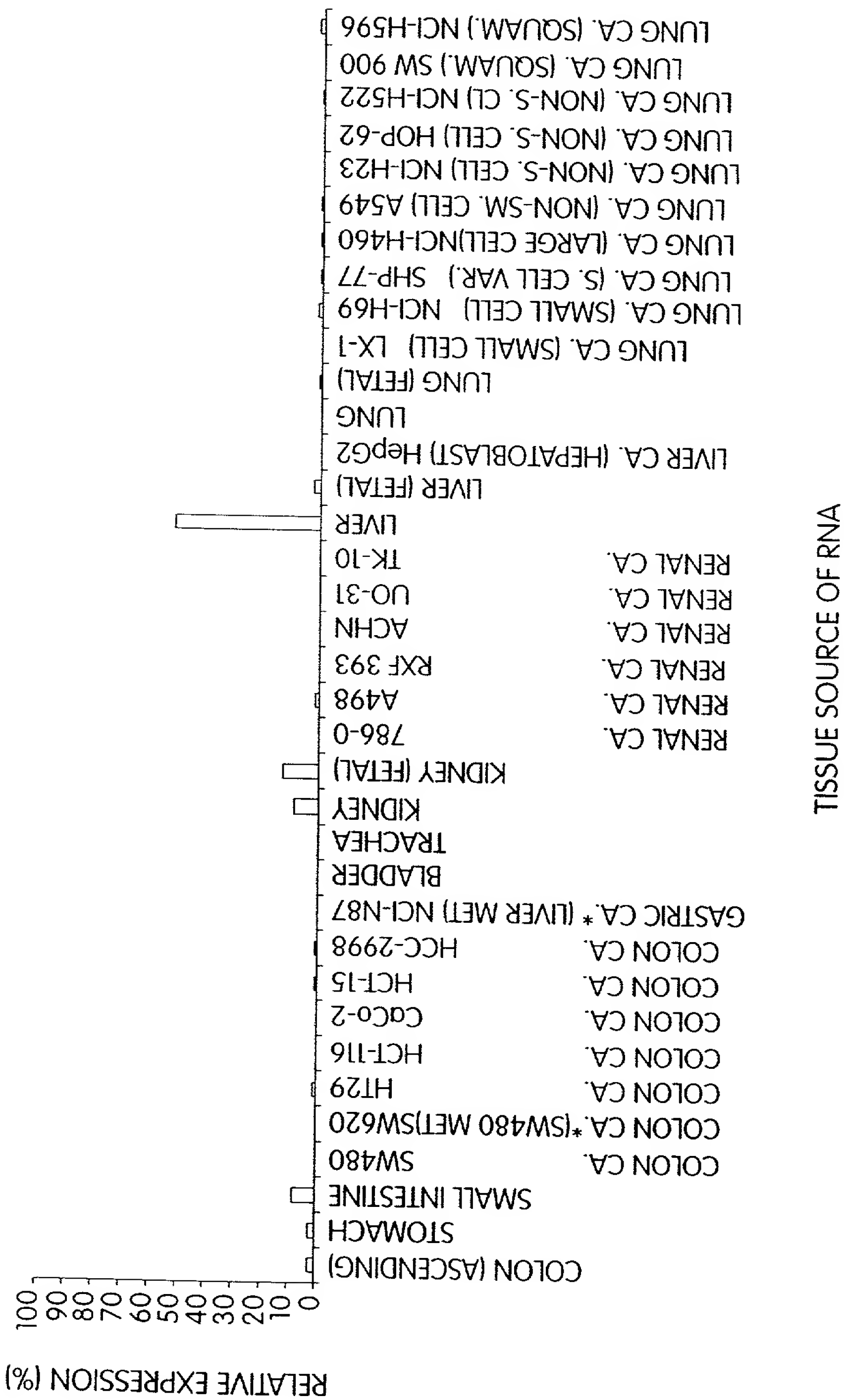

Fig. 20 (PANEL B)

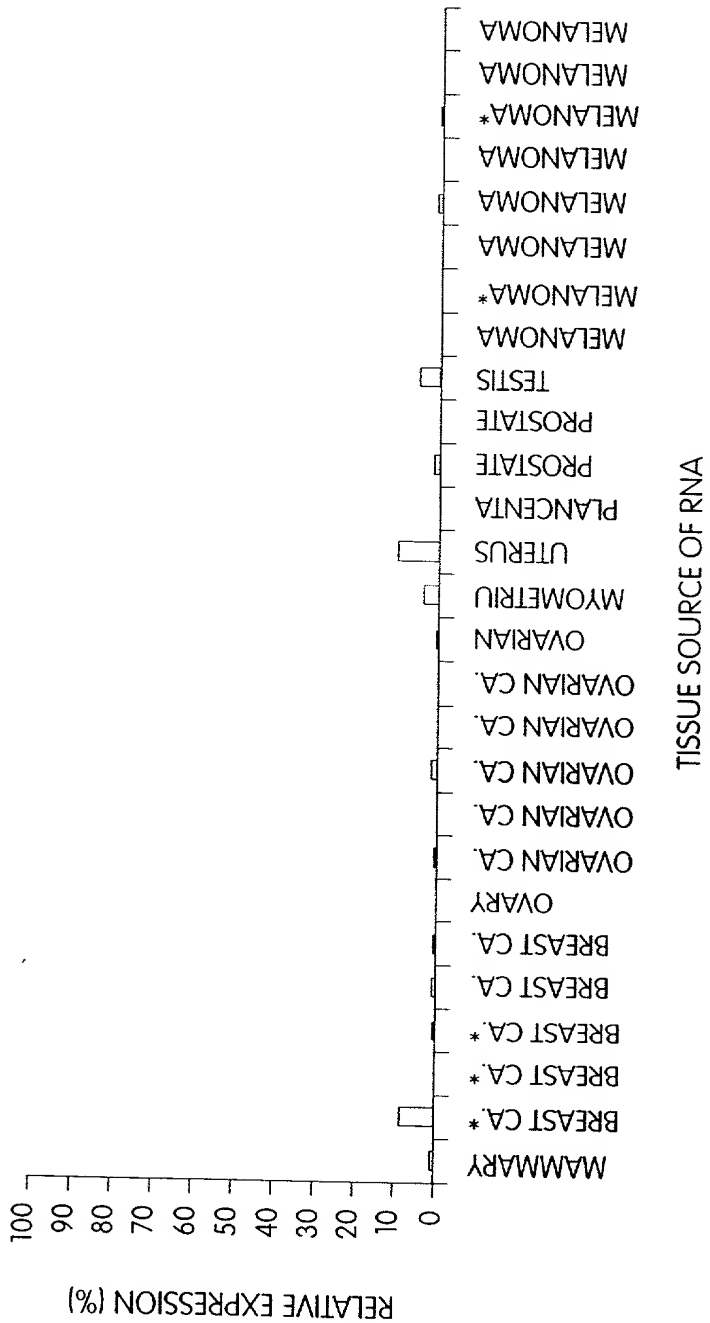

Fig. 20 (PANEL C)

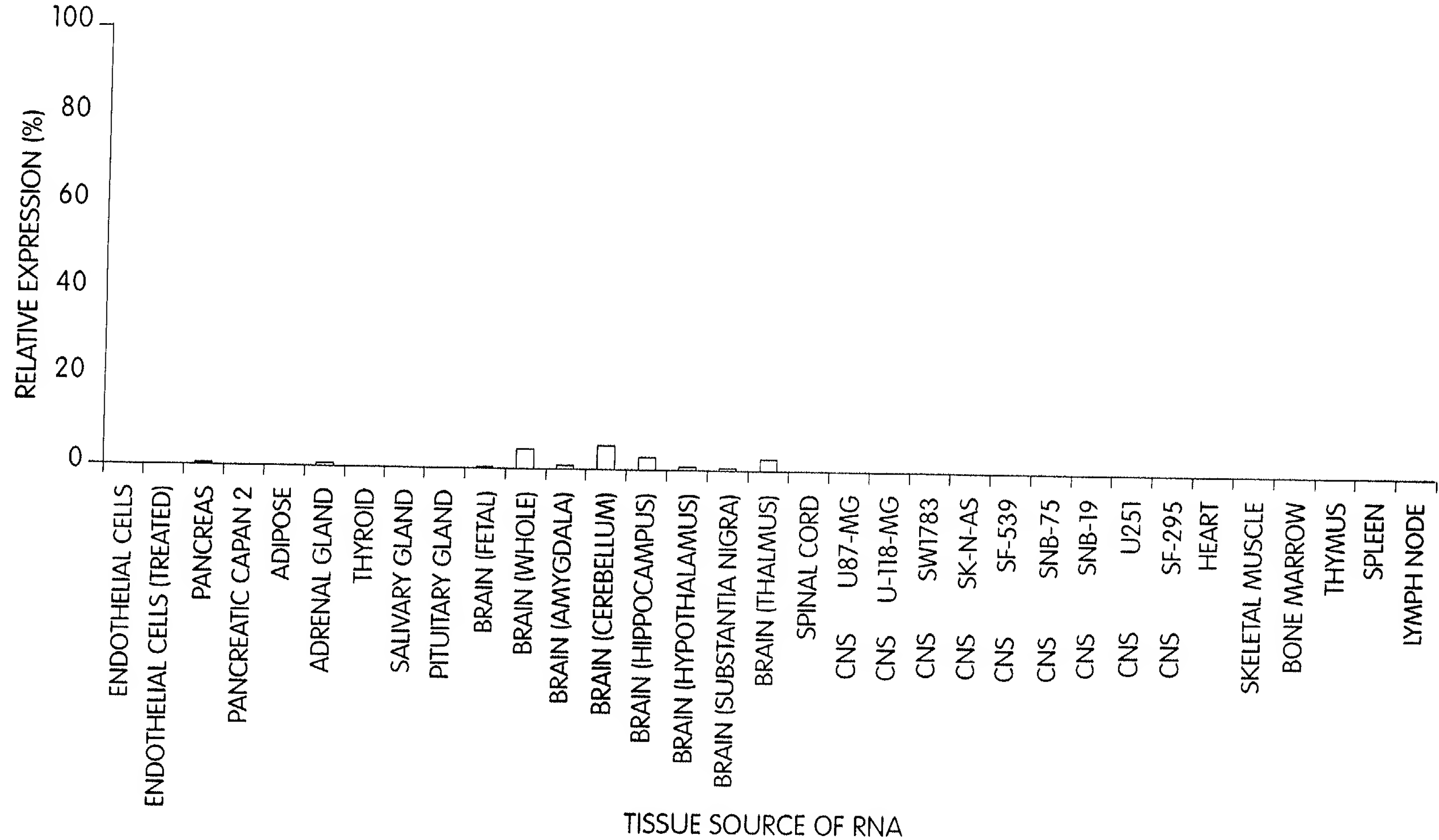

Fig. 21 (PANEL A)

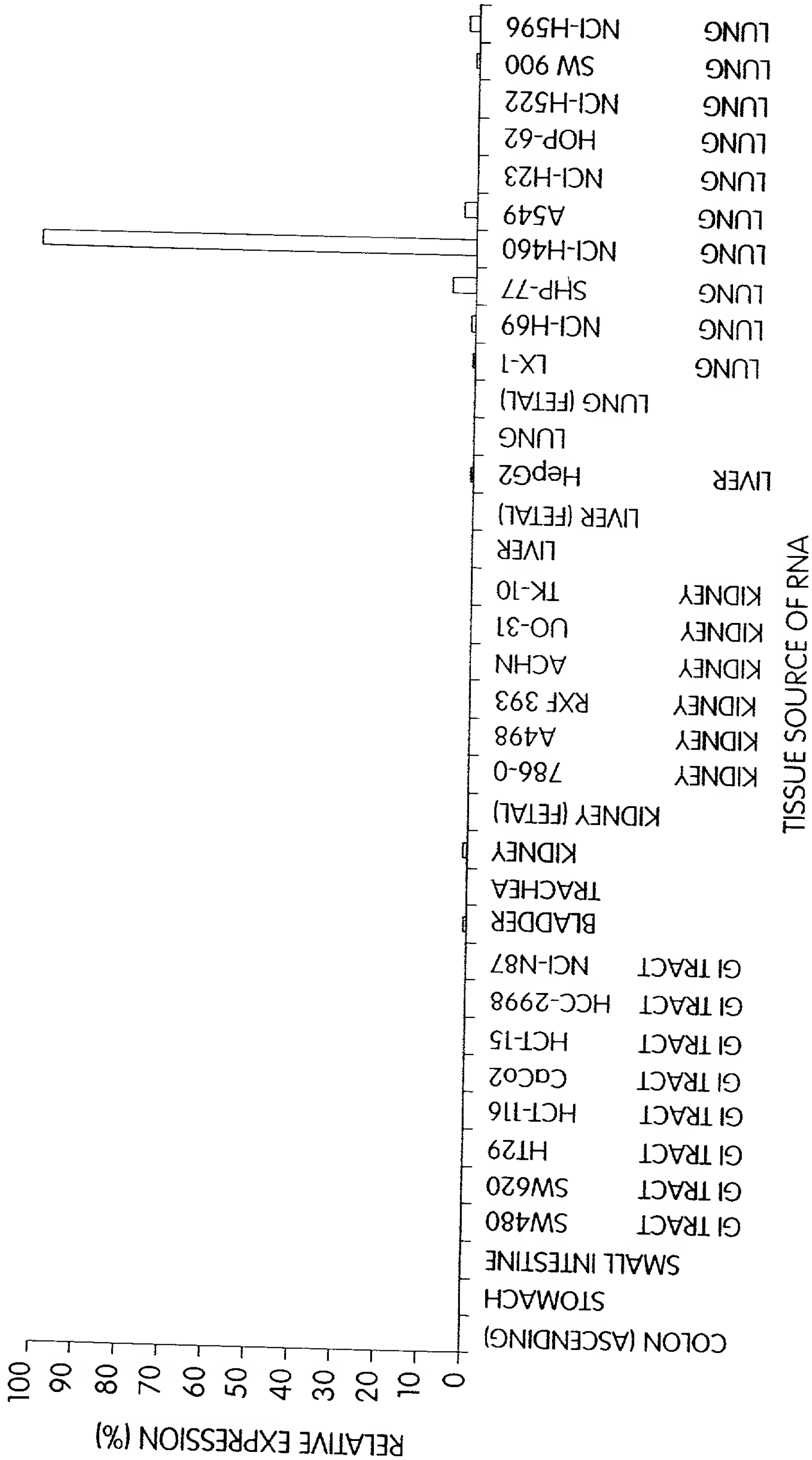

Fig. 21 (PANEL B)

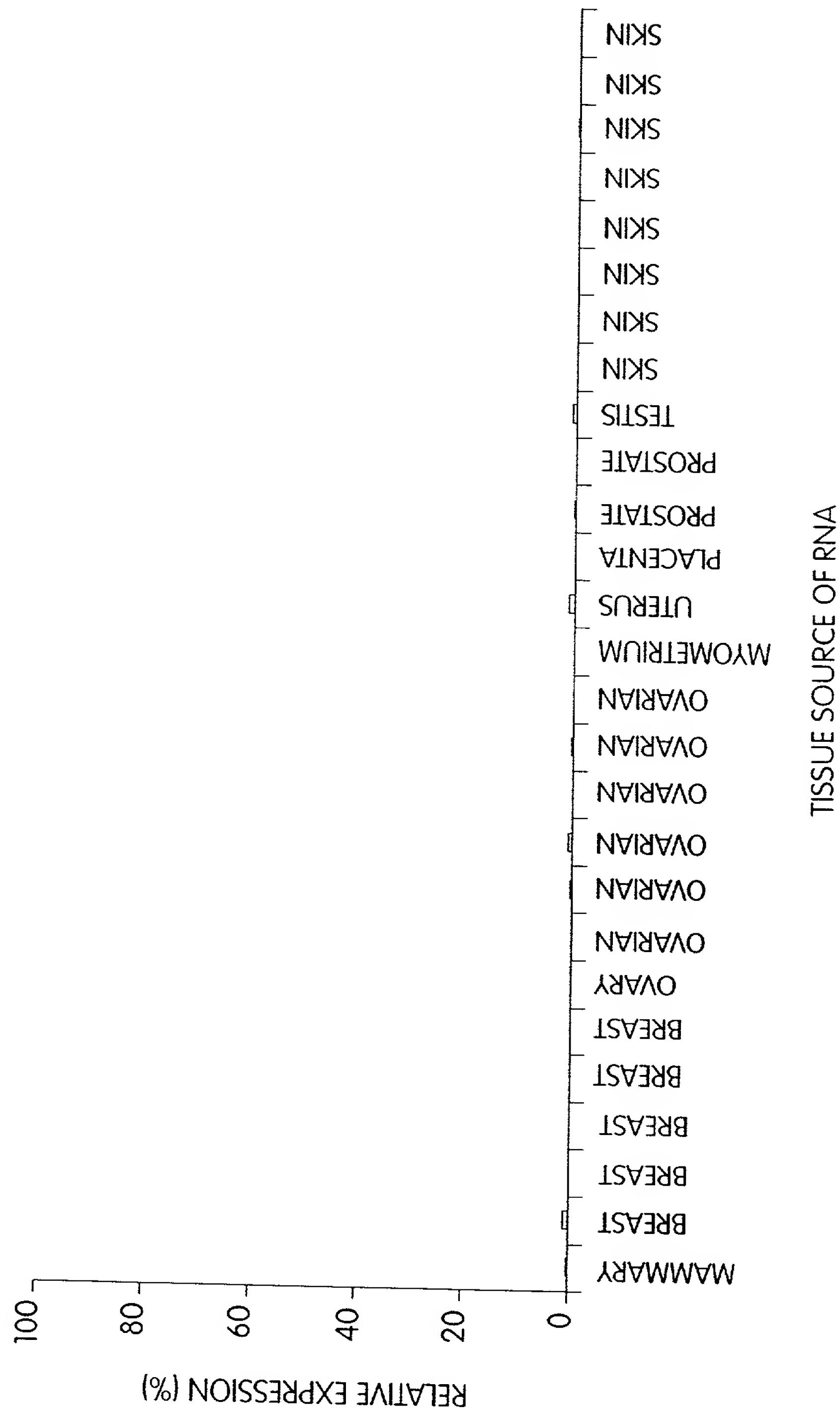

Fig. 21 (PANEL C)

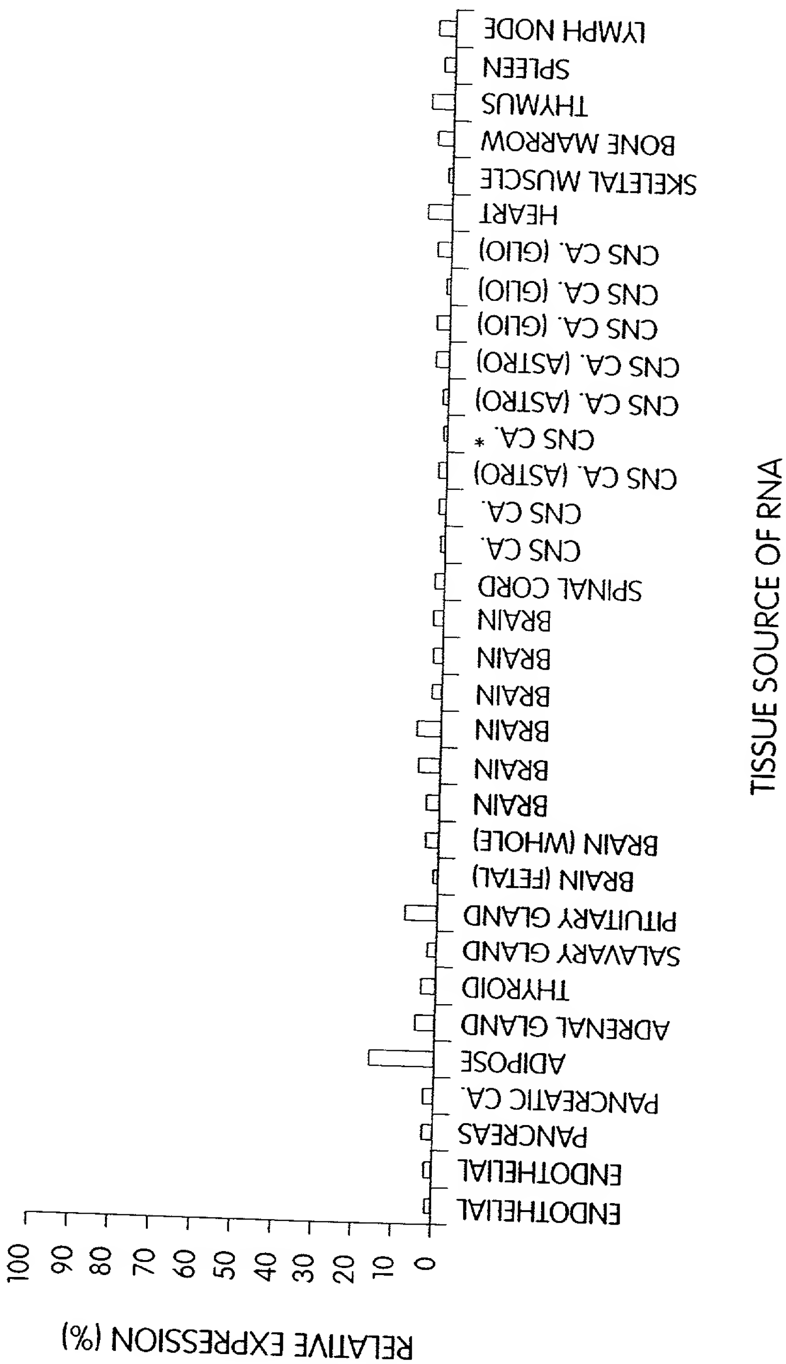

Fig. 22 (PANEL A)

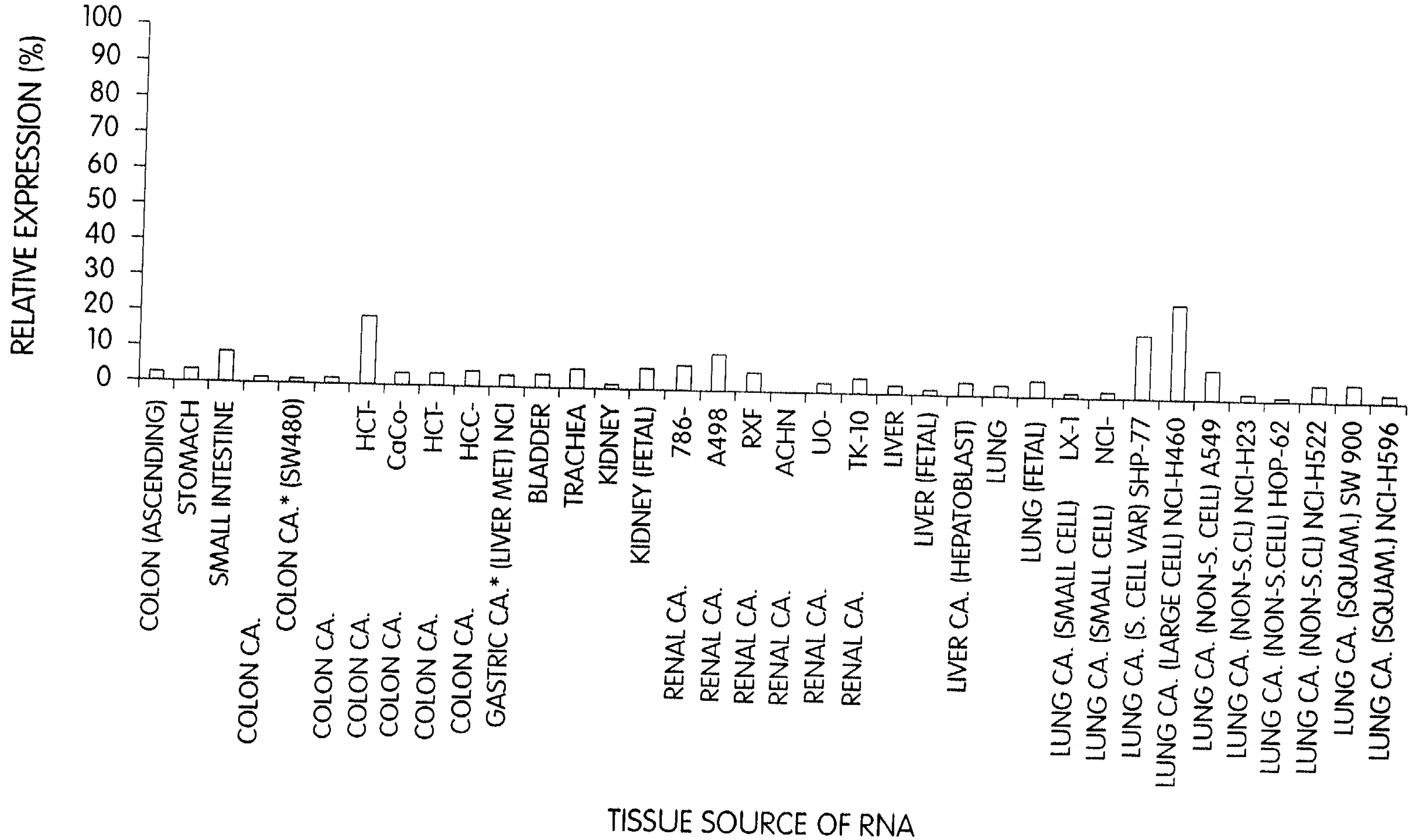

Fig. 22 (PANEL B)

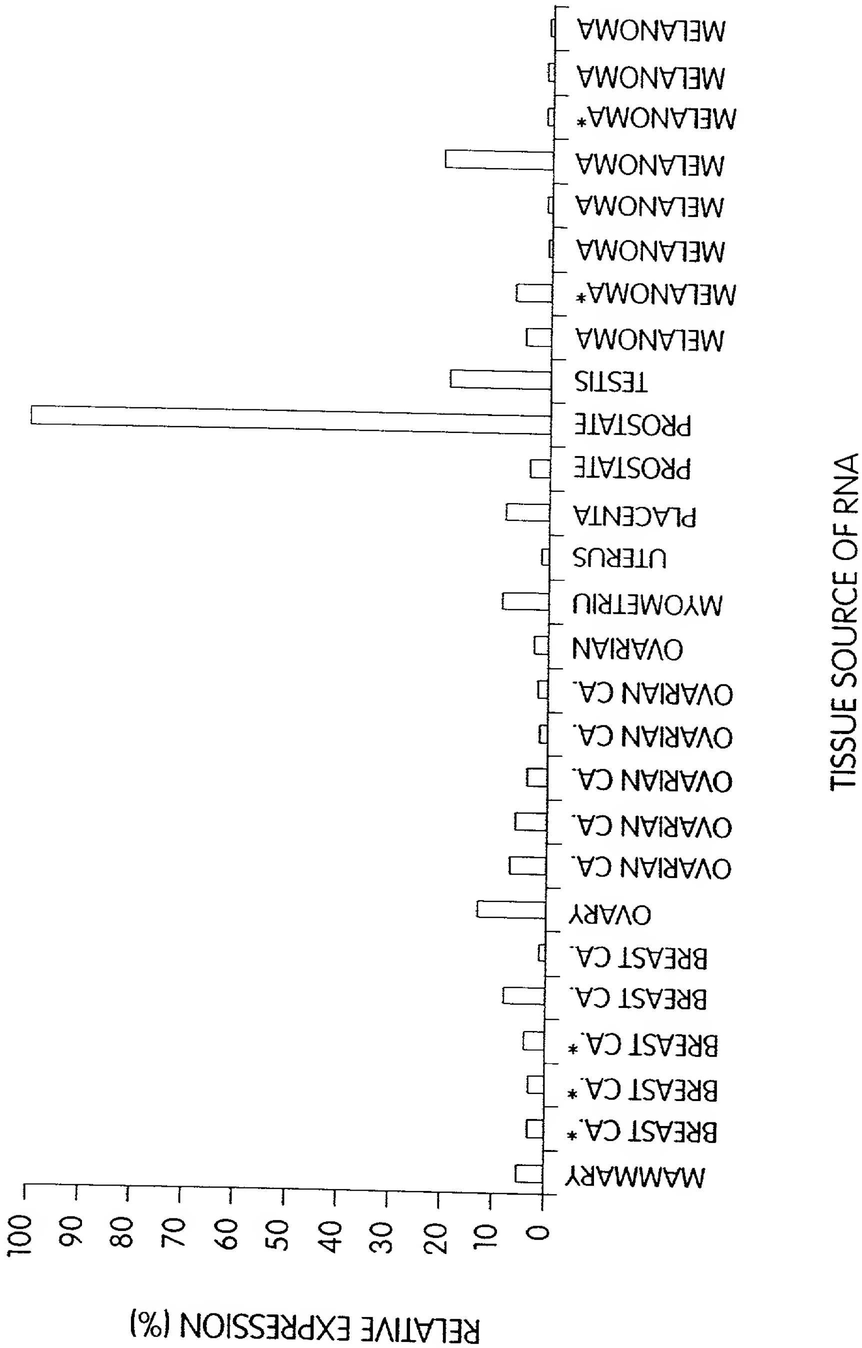

Fig. 22 (PANEL C)

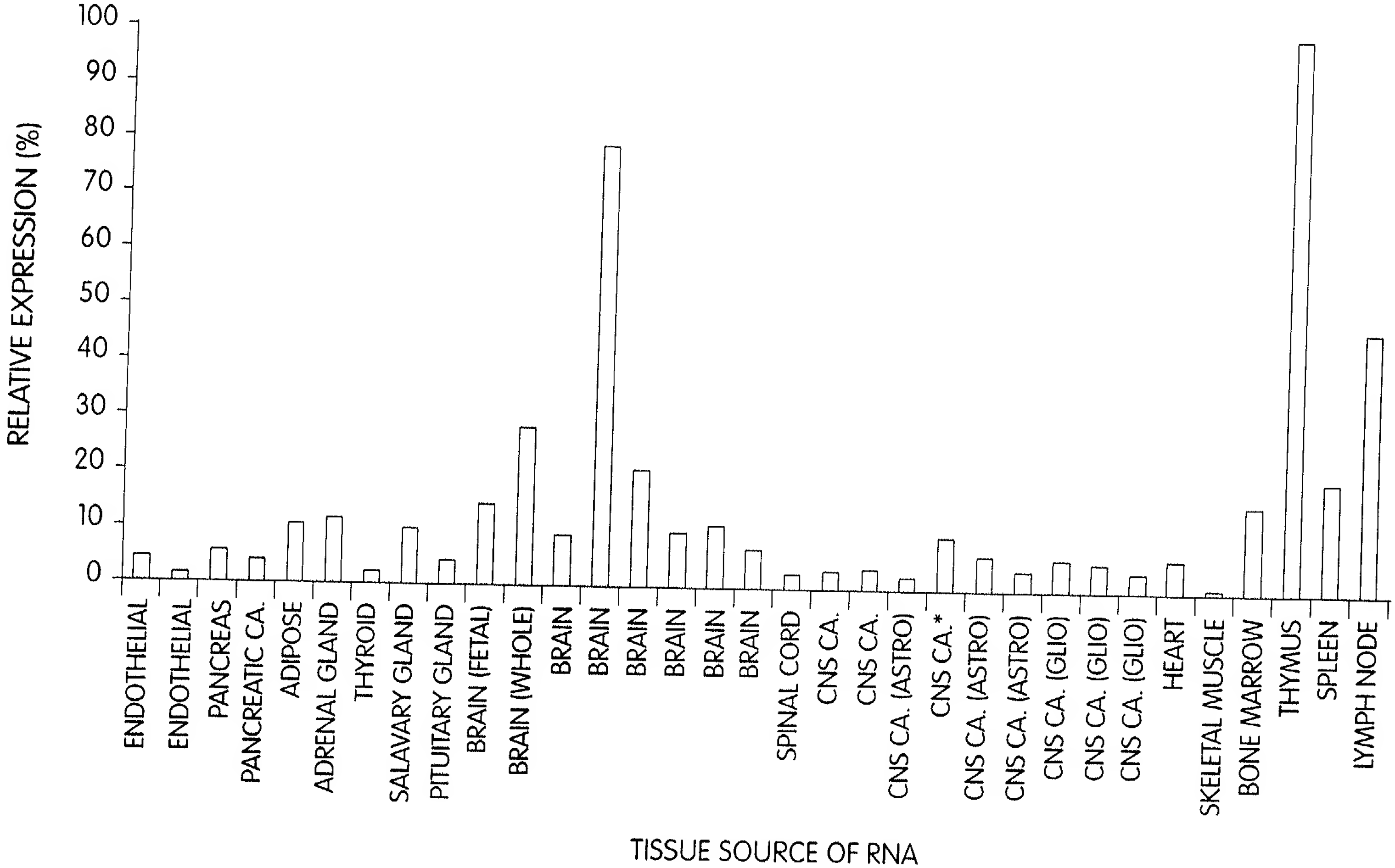

Fig. 23 (PANEL A)

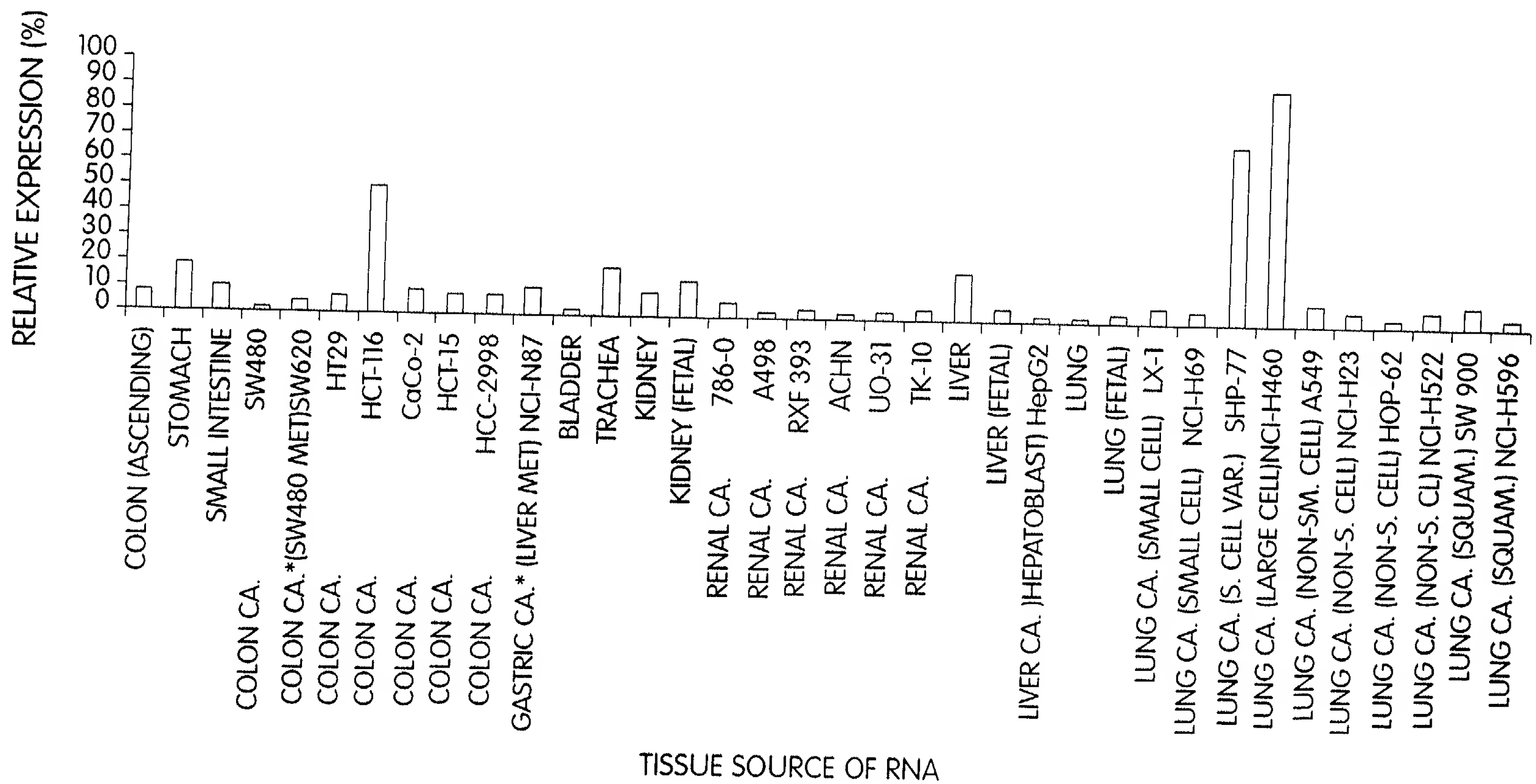

Fig. 23 (PANEL B)

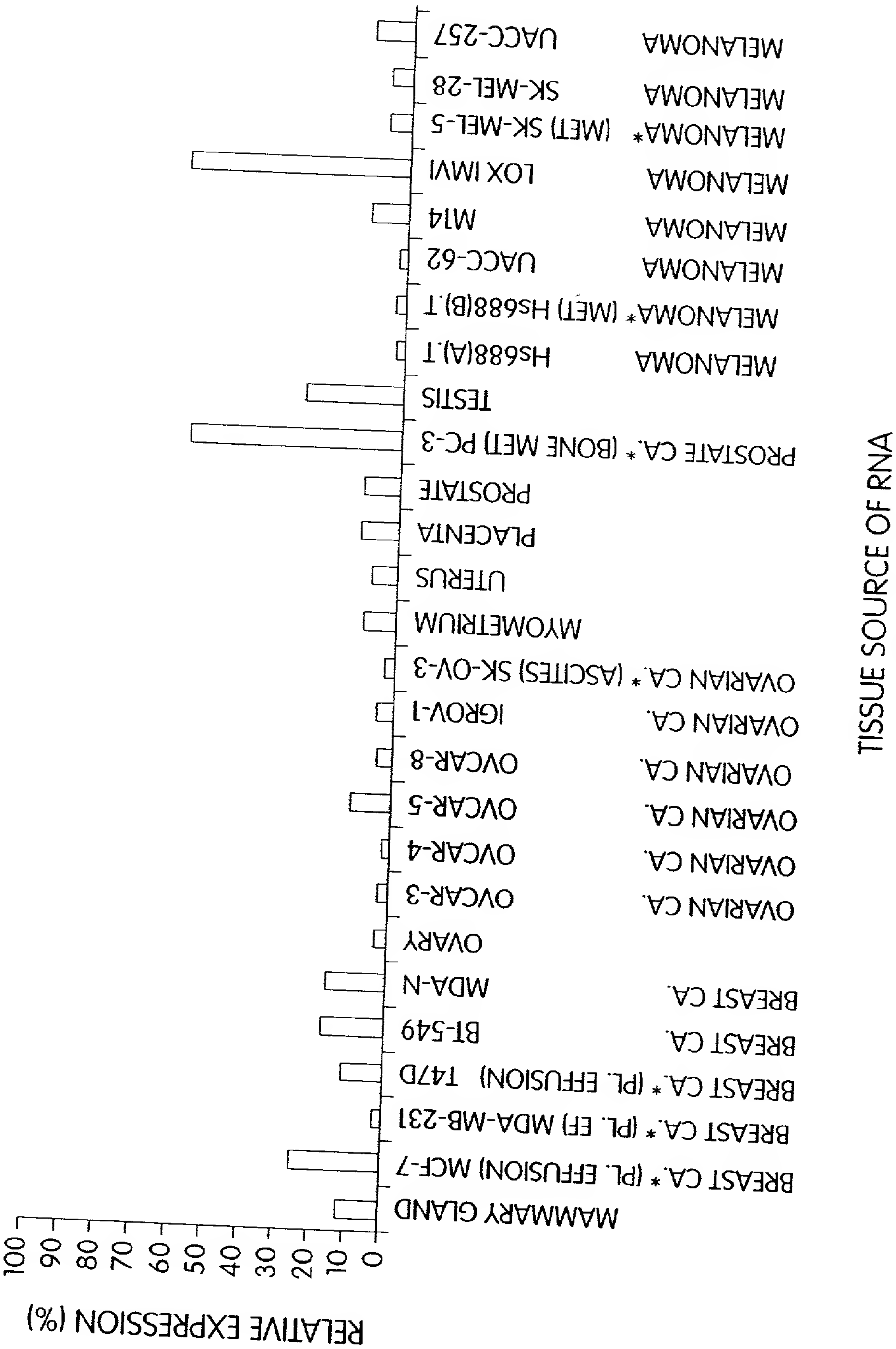

Fig. 23 (PANEL C)